

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 15, 2003, 21:11:36 ; Search time 2164.55 Seconds
(without alignments)
3925.989 Million cell updates/sec

Title: US-09-624-670-63
Sequence: 1 MBOLKAFIDNEVNAFLDNMFG.....NGPKAHILVANGMTDKKAAQ 292

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Zgapop 6.0 , Zgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-UNIT=ICN=200 -THR_SCORE=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTTEMP=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THRAUD=10 -XGAPEXT=0.5 -PGAPOP=6
-PGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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pred No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	1567	100.0	879	6	AX464734	AX464734 Sequence
2	1567	100.0	3708	10	AF170908	AF170908 Mus muscu
3	1567	100.0	3795	6	AX052773	AX052773 Sequence
4	1430	91.3	2340	9	AK000341	AK000341 Homo sapi
5	960.5	64.3	2702	10	BC022911	BC022911 Mus muscu
6	958.5	61.2	900	10	AB071985	AB071985 Rattus no
7	958.5	61.0	900	6	AX464735	AX464735 Sequence
8	951.5	60.7	2757	9	HS0801903	HS0801903 Homo sapi
9	951.5	60.7	3011	9	AF338241	AF338241 Homo sapi
10	946.5	60.4	900	9	AF231981	AF231981 Homo sapi
11	941.5	60.1	914	6	AX464732	AX464732 Sequence
12	919.5	58.7	2592	6	IO3465	IO3465 Sequence 1
13	919.5	58.7	2592	6	IO3465	IO3465 Sequence 1
14	910	58.1	1397	5	AF455250	AF455250 Scophthal
15	691.5	44.1	975	5	AX127458	AX127458 Sequence
16	679	43.3	945	9	AK055277	AK055277 Homo sapi
17	679	43.3	2219	9	AK055277	AK055277 Homo sapi
18	679	43.3	2900	9	AF277034	AF277034 Homo sapi
19	679	43.3	3272	9	AY037284	AY037284 Homo sapi
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21	679	43.3	3583	6	AX430266	AX430266 Sequence
22	663.5	42.3	3415	6	AX402493	AX402493 Sequence
23	663.5	42.3	2868	10	AF277093	AF277093 Mus muscu
24	621	36.6	288539	14	AF198100	AF198100 Fowlpox v
25	531.5	33.9	846	6	AX467489	AX467489 Sequence
26	525.5	33.5	1986	3	AY119173	AY119173 Drosophil
27	495	33.1	2580	3	AY060267	AY060267 Drosophil
28	495	31.8	86594	5	AC095019	AC095019 Rattus no
29	495	31.6	2508	9	AK027216	AK027216 Homo sapi
30	493.5	31.5	1830	10	LC005002	LC005002 Mus muscu
31	464	29.6	2018	3	AY113567	AY113567 Drosophil
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41	435	27.8	1595	3	AF005682	AF005682 Drosophil
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C 43	419.5	26.8	173782	3	AC096692	AC096692 Drosophil
C 44	419.5	26.8	281602	3	AF003546	AF003546 Drosophil
C 45	407.5	26.0	50374	2	AC015170	AC015170 Drosophil

ALIGNMENTS


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221 LeuSerAlaValValLysProGlyGlyPheProPheGlyLysLeuLeuLeuSerSer 240
697 CTGAGTGGCGGCGTGAAGAGCTGTGGTTCCTGCTTGGCTGTCTATCTCTCAAGTGTTC 756
241 TyrMetMetPheLeuValLysLeuPheLeuAsnPheTyrIleGlnThrTyrTATATLysLys 260
757 TATATGATGAGAGTGGTCACTCTCTTATATATCTATATTCAGACATACAGGAGAGAG 816
241 ProValLysLysGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 280
817 CTACGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 876
281 IleValAlaAsnGlyMetThrAspLysGlnAlaGln 292
877 ATTGTGGTAAATGATATATATATATATATATATATATATATATATATATATATATAT 912

RESULTS 4
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LOCUS Homo sapiens cDNA FLJ20334 f1s, clone HEP11362.
ACCESSION AK000441
VERSION AK000441.1 GI:7020360
KEYWORDS oligo capping; f1s (full insert sequence).
SOURCE Homo sapiens hepatoma cell_line: HepG2 cDNA to mRNA, clone_f1b: HEP
clone: HEP11362.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (sites)
Kawakami, T., Nonuechi, S., Itoh, T., Shigeta, K., Senba, T.,
Matsumura, K., Nakajima, Y., Mizuno, T., Morinaga, M., Ota, T.,
Suzuki, Y., Okeyashi, M., Nishi, T., Shibahara, T., Tanaka, T.,
Nakamura, Y., Isoqali, T. and Sugano, S.
NEBO human cDNA sequencing project
Unpublished
2 (bases 1 to 2440)
Sugano, S., Suzuki, Y., Ota, T., Okeyashi, M., Nishi, T., Isoqali, T.,
Shibahara, T., Tanaka, T. and Nakamura, Y.
Direct Submission
Submitted (15-FEB-2000) Sumio Sugano, Institute of Medical Science,
University of Tokyo, Department of Virology, Shirokane-dai, 4-6-1,
Minato-ku, Tokyo 108-8639, Japan (E-mail: csdnalabs.u-tokyo.ac.jp,
Tel: 81-3-5449-5286, Fax: 81-3-5449-5416)
NEBO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; cDNA full insert
sequencing: Research Association for Biotechnology; cDNA library
construction, 5' & 3' end one pass sequencing: Department of
Virology and Human Genome Center, Institute of Medical Science,
University of Tokyo (partly supported by Science and Technology
Agency).
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BASE COUNT 686 a 504 c 459 g 691 t

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ORIGIN

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Best Local Similarity: 88.18% Mismatches: 14
Query Match: 91.26% Indels: 4
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QY 261 ProValLysLysGlnLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 276
DB 865 CCAATCAACAAGATATGCAAGACAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAG 924
QY 277 LysAlaHisLeuLeuValAlaAsnGlyMetThrAspLysLysAlaGln 292
DB 925 AAAGGTTATCTTCACTGTGAGTAAATGAGAGTGTATGAGTAAAGTAAAGTAAAGTAAAGTAA 972

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RESULT 5

BC022911 mRNA linear pop 07-Aug-2002
 MUS musculus, clone MCC:27526 IMAGE:4457285, mRNA, complete cds.
 BC022911 GI:18605604
 MGC:
 house mouse.
 Mus musculus
 Fukuyota, Metazoa; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 (bases 1 to 2702)
 Strausberg,K,ision
 Direct Submit(04-FEB-2002) National Institutes of Health, Mammalian
 Genome Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: http://mgc.nci.nih.gov
 Contact: MGC help desk
 Email: cgapbs@mail.nih.gov
 Tissue Procurement: Gilbert Smith, Ph.D.
 cDNA Library preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
 DNA Sequencing by: Baylor College of Medicine Human Genome
 Sequencing Center
 Center code: BCM-HGSC
 Web site: http://www.hgsc.bcm.tmc.edu/cdna/
 Contact: amg@bcm.tmc.edu
 Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
 Yoon, V.S., Kuo, C.P., Lawrence, S., Martin, R.G., Muzny, D.M.,
 Richards, S., Gibbs, R.A.
 Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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 This clone was selected for full length sequencing because it
 passed the following selection criteria: Hexamer frequency ORF
 analysis, similarity but not identity to protein.
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 /map="FVB/N"
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 /vector="pCMV-Sport6"
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Best Local Similarity:	61,30%	Indels:		3
Query Match:	10	Gaps:		1
db:				

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[illegible]

Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo.

REFERENCE
AUTHORS Mukerji, P., Das, T., Huang, Y.S., Parker, Barnes, J.M., Leonard, A.E.,
Thurmond, J., and Pereira, S.L.
TITLE Elouage genes and uses thereof
JOURNAL Patent: WO 02/040401 A3 31-JAN-2002
FEATURES
SOURCE Abbott Laboratories (US)
location/qualifiers
L: 914
/organism: "Homo sapiens"
/db xref: "taxon:9606"
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US 09-624 670-63 (1-292) x AX464742 (1-914)

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QY 283 AlaAsnGlyMetThrAsp 288
DB 829 GTGANTGGATCAACCAAC 846

RESULT 12
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ACCESSION 105465
VERSION 105465.1 GI:590717
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2592)
AUTHORS Ishizaka, K., Martens, C.L., and Moore, K.W.
TITLE Glycosylation inhibition factors
JOURNAL Patent: EP 0284095-A1 1 05 OCT 1988.
FEATURES
location/qualifiers
L: 2592
/organism: "unknown"
BASE COUNT 684 a 575 c 548 g 785 t
ORIGIN

Alignment Scores:
Pred. No.: 556 74 Length: 2592
Score: 919.50 Matches: 169
Percent Similarity: 72.19% Conservative: 70
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Query Match: 58.68% Indels: 4
DB: 6 Gaps: 2

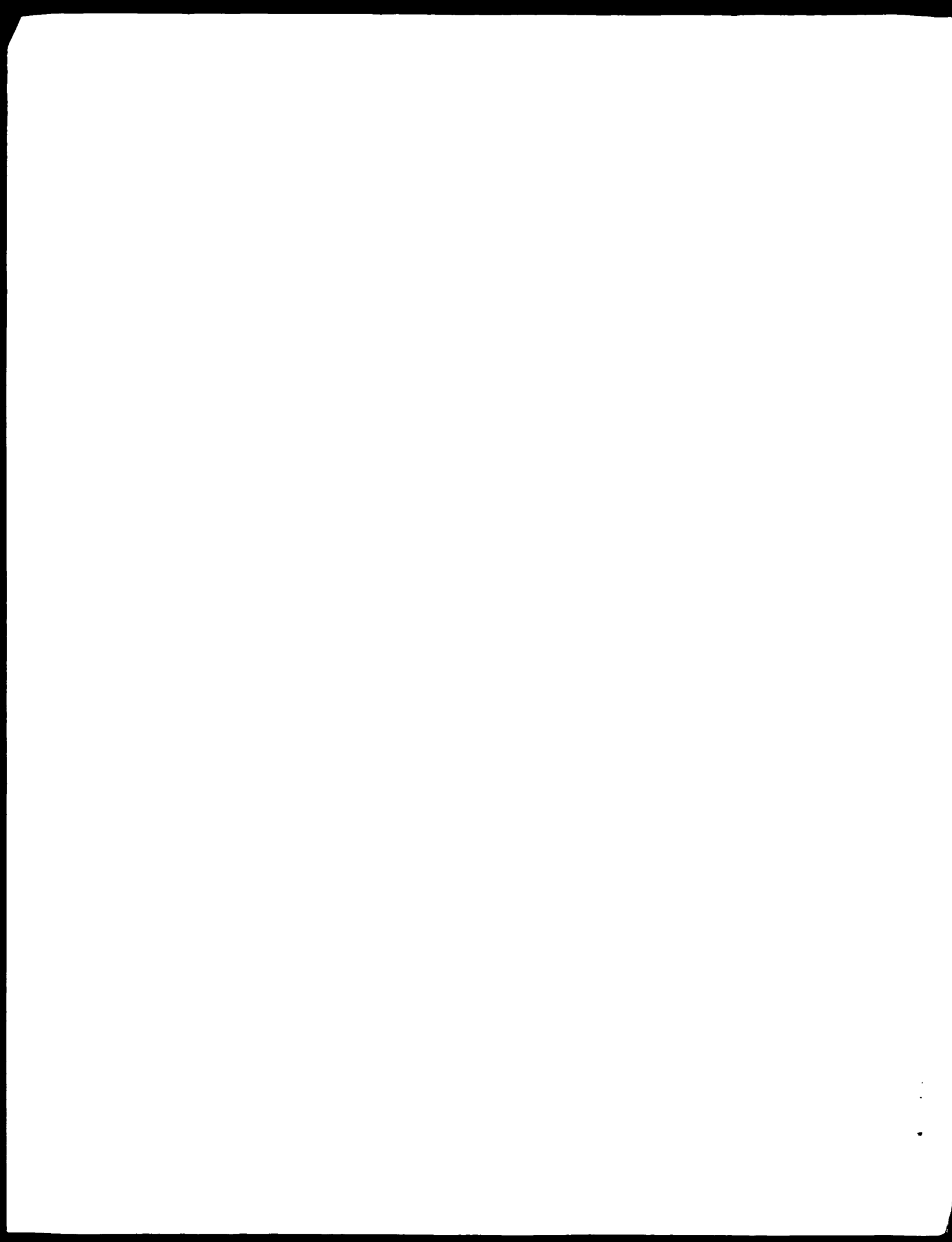
US 09-624-670-63 (1-2592) x 105465 (1-2592)

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 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 2592)
 AUTHORS Ishizaka, K., Martens, C. L. and Moore, K. W.
 JOURNAL Patent WO 8807577-A 1 06-OCT-1988;
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 Query Match: 58.68% Indels: 8
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 QY 153 MetPheAsnIleTyrTrpCysValLeuAsnTrpIleProCysGlyGlnSerPheGly 172
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 DB 490 GGCACACTCAACAGCTTAT 549
 QY 193 ProSerMetHisTyrLeuTrpTyrPheLysTyrLeuThrGlnAlaGlnLeuValGln 212
 DB 550 GGTGATATGCTTATATGCTTATATGCTTATATGCTTATATGCTTATATGCTTATATGCT 609
 QY 213 PheValLeuThrLeuHisThrLeuSerAlaValValTyrProCysGlyPheProPhe 232
 DB 610 TTGTCGTCGACAAAT 669
 QY 233 GlyCysLeuLeuPheGlnSerTyrMetThrLeuValLeuValLeuValLeuValLeu 252
 DB 670 GGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 729
 QY 253 TyrTyrGlnThrTyrArgTyrValTyrValTyrValTyrValTyrValTyrValTyr 272
 DB 730 TACATTCAT 780
 QY 273 AsnGlyPheProLysAlaHisLeuValAlaValValValValValValValValVal 288
 DB 781 AAGGGCAAT 828
 RESULT 14
 LOCUS AF465520
 DEFINITION Scophthalmus maximus polyunsaturated fatty acid elongase (ELO)
 ACCESSION AF465520
 VERSION AF465520.1 GI:18448974
 KEYWORDS
 SOURCE Scophthalmus maximus.
 ORGANISM Scophthalmus maximus.
 REFERENCE 1 (bases 1 to 1397)
 AUTHORS Ajaba, M. K., Kocher, D. P., Buckman, C. A. and Teale, A. J.
 TITLE Polyunsaturated fatty acid elongase from teleost fish
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1397)
 AUTHORS Ajaba, M. K., Kocher, D. P., Buckman, C. A. and Teale, A. J.
 TITLE Direct Submission
 JOURNAL Submitted (03-JAN-2002) Institute of Aquaculture, University of Stirling, Stirling FK9 4LA, UK
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GenCore version 5.1.6
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QM protein - nucleic search, using frame_plus_p2n model

Run on: June 15, 2003, 20:25:36 ; Search time 201.944 seconds
(without alignments)
3262.066 Million cell updates/sec

Title: US-09-624-670-63

Perfect score: 1567
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Scoring table:

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 2185239 seqs, 112599459 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB	ID	Description
1	1567	100.0	879	24	ABK46369	Mouse elongase MEL
2	1567	100.0	3795	22	AAK91702	Mouse fatty acid e
3	1431	91.3	3645	23	ABV22609	Human prostate exp
4	1431	91.3	3645	23	ABV24286	Human prostate exp
5	1431	91.3	3645	23	ABV28431	Human prostate exp
6	956.5	61.0	900	24	ABK46370	Mouse elongase MEL
7	951.5	60.7	2001	23	ABV23421	Human prostate exp
8	951.5	60.7	2001	23	ABV24778	Human prostate exp
9	951.5	60.7	2001	23	ABV25364	Human prostate exp
10	951.5	60.7	2001	23	ABV29278	Human prostate exp
11	951.5	60.7	2313	21	AAK64369	Human vesicle asso
12	951.5	60.7	5627	22	AAK94320	Human full-length
13	951.5	60.7	2769	22	AAK44747	Human full-length
14	951.5	60.7	5083	22	AAK44919	Human contig polyn
15	947.5	60.5	2710	21	AAK54132	Breast cancer prot
16	946.5	60.4	914	21	AAK294241	Human elongase HSE
17	941.5	60.1	914	24	ABK46367	Human elongase HSE
18	921	58.8	1907	24	ABL90374	Human polynucleoti
19	863	55.1	2571	9	AAH81168	Fragment from clon
20	749	47.8	748	22	AAK27317	cDNA encoding nove
21	741	47.3	680	22	AAK91344	Human CDNA 5'-end
22	741	47.3	680	22	AAK93349	Human CDNA clone r
23	691.5	44.1	975	22	AAU07430	Human cold-induced
24	679	43.3	972	24	AAK19305	Human elongation o
25	679	43.3	1203	23	AAK91595	DNA encoding novel
26	679	43.3	3383	24	ABQ72496	Human MDR1 encodin
27	679	43.3	3415	24	ABK28654	Human CDNA encodin
28	670.5	42.8	871	22	AAK27318	cDNA encoding nove
29	663.5	42.3	1292	24	AAK19307	Mouse elongation o
30	650	41.5	967	24	AAK19306	Human elongation o
31	600	38.3	2224	24	ABQ75877	Pescadillo protein
32	579.5	37.0	817	24	AAK93682	Human CDNA clone r
33	506.5	32.3	1914	23	ABH15699	Drosophila melanog
34	476.5	30.4	883	23	ABH105185	Drosophila melanog
35	465	29.7	888	23	ABH109165	Drosophila melanog
36	464.5	29.6	1329	23	ABH10787	Drosophila melanog
37	462.5	29.5	1472	24	ABQ91925	Human NF-KB activa
38	462.5	29.5	1482	19	AAV59752	Human secreted pro
39	462.5	29.5	1514	24	AAI45857	Human secreted pro
40	462.5	29.5	1542	19	AAV59606	Human secreted pro
41	462.5	29.5	1566	21	AAZ56736	Human transmembran
42	460.5	29.4	1457	22	AAH14551	Human CDNA sequenc
43	457.5	29.2	969	22	AAK91701	Human fatty acid e
44	457.5	29.2	1468	22	AAK91700	Mouse fatty acid e
45	455.5	29.1	1083	23	ABH09223	Drosophila melanog

ALIGNMENTS

RESULT 1
ID ABK46369 standard; cDNA, 879 BP.
XX
AC ABK46369;
XX
DT 05-JUN-2002 (first entry)
XX
DE Mouse elongase MEL04 cDNA.

ss: gene; elongase; polyunsaturated fatty acid; pufa; transgenic plant;
transgenic non-human animal; plant oil; arachidonic acid; nutritional;
pharmacut-cal; cosmetic; animal feed; testenosis; angioplasty; AIDS;
acquired immunodeficiency syndrome; multiple sclerosis; cachexia; asthma;
inflammatory skin disease; osteoporosis; kidney stone; cancer; eczema;
inflammation; rheumatoid arthritis; psoriasis; platelet aggregation;
vasodilation; cholesterol reduction; gastrointestinal bleeding.
XX

[illegible]

QY	101	Asn	Leu	Asp	Ser	Ala	Gly	Glu	Gly	Asp	Val	Arg	Val	Ala	Val	Leu	Trp	Trp	Tyr	120
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QY	121	Phe	Ser	Trp	Ser	Leu	Val	Glu	Phe	Leu	Asp	Thr	Ile	Phe	Phe	Phe	Val	Leu	Arg	140
DB	397	TT	CT	CA	AAA	CT	AG	TGG	AG	AT	TC	TGG	AC	CA	CA	AT	TT	CT	TT	456
QY	141	Gln	Ile	Thr	Phe	Leu	His	Val	Tyr	His	His	Ala	Ser	Met	Phe	Asn	Ile	Trp	Trp	160
DB	457	CAG	ATC	AC	CT	TC	CT	CA	TG	CT	AT	CA	CAC	CG	CT	CC	AT	GT	CA	516
QY	161	Leu	Asn	Trp	Ile	Pro	Cys	Gly	Gln	Ser	Phe	Phe	Gly	Pro	Thr	Leu	Asn	Ser	Phe	180
DB	517	TT	GAA	CT	GA	AT	CT	TT	GG	TC	CA	AA	AG	TT	CT	TT	TT	TT	TT	576
QY	181	Ile	Leu	Met	Tyr	Ser	Ile	Ser	Ile	Gly	Leu	Ser	Val	Phe	Pro	Ser	Met	His	Ser	200
DB	577	AT	CT	CA	AT	GA	CT	CC	TA	CA	AG	GC	CT	CT	CT	CT	CT	CT	CT	636
QY	201	Trp	Ile	Ser	Tyr	Leu	Thr	Gln	Ala	Gln	Leu	Val	Gln	Phe	Val	Leu	Thr	Ile	Thr	220
DB	637	TGG	AAG	AG	TAC	CT	CA	CAC	AGG	CT	CAC	TGG	TGC	AG	CT	TCT	CT	CT	CT	696
QY	221	Leu	Ser	Ala	Val	Val	Lys	Pro	Cys	Gly	Phe	Pro	Phe	Gly	Cys	Leu	Ile	Phe	Gln	240
DB	697	CT	AG	AT	GC	CT	GG	CT	GG	CT	GG	CT	GG	CT	GG	CT	GG	CT	GG	756
QY	241	Tyr	Met	Met	Thr	Leu	Val	Ile	Leu	Phe	Leu	Asn	Phe	Tyr	Ile	Gln	Thr	Tyr	Arg	260
DB	757	TA	AT	GA	TAC	AG	CT	GG	CT	CA	CT	CT	CT	CT	CT	CT	CT	CT	CT	816
QY	261	Pro	Val	Lys	Lys	Glu	Leu	Gln	Lys	Glu	Val	Lys	Asn	Gly	Phe	Pro	Lys	Ala	His	280
DB	817	CC	AG	TC	GA	GA	AA	AG	AG	CT	TC	CA	AG	AA	GA	AG	TA	GT	TT	876
QY	281	Ile	Val	Ala	Asn	Gly	Met	Thr	Asp	Lys	Lys	Ala	Gln	292						
DB	877	ATT	GT	GG	TA	AT	GC	AT	GA	TA	GA	AA	GA	TA	GA	AA	GA	TA	GA	932
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XX	13	Ser	2002	(first	entry)															
XX	Human	prostate	expression	marker	CDNA	22609														
XX	Human	prostate	cancer	cytostatic	carcinogen	pharmacodynamic	marker													
XX	Human	prostate	cancer	cytostatic	carcinogen	pharmacodynamic	marker													
XX	Human	prostate	cancer	cytostatic	carcinogen	pharmacodynamic	marker													
XX	Homo	sapiens																		
XX	W020016	(085C-A2)																		
XX	24-AUG-2001																			
XX	20-FEB-2001	2000US-US051171					</													

WP1: 2001 662795/76.

Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer.

Claim 1; Page 3958; 11750pp; English.

The invention relates to an isolated nucleic acid molecule (1) comprising a nucleotide sequence given in Tables 1-9 (ABV62213) of the specification or its complement. (1) is useful for:

(a) assessing whether a patient is afflicted with prostate cancer;

(b) monitoring the progression of prostate cancer in a patient;

(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;

(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;

(e) selecting a composition for inhibiting prostate cancer in a patient;

(f) assessing the prostate cell carcinogenic potential of a compound;

(g) determining whether prostate cancer has metastasized in a patient;

(h) assessing the aggressiveness or indolence of prostate cancer in a patient;

(i) is also useful as a pharmacodynamic or pharmacogenomic marker.

Sequence 3645 BP: 1041 A: 793 C: 684 G: 1114 T: 8 other;

Alignment Scores:

Pred. No.: 5,466 109 Length: 3645

Score: 141100 Matches: 262

Percent Similarity: 93.92% Conservat: 16

Best Local Similarity: 88.51% Mismatches: 14

Query Match: 91.42% Indels: 4

DB: 23 Gaps: 1

US 09-624-670-63 (1-292) x ABV:22609 (1-3645)

QY 1 MetGluGlnGluValAlaPheAspAsnGluValAsnAlaPheLeuAspAsnMetPheGly 20
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DB 85 ATGGANATCTAAGAGCTTTTGATGATGAATAAATGCTTTTGGACAAATATGTTTGA 144
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QY 21 ProArgAspSerAvalAlaGlyTyrPheLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 40
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DB 145 CGGACAGATGCTGACAGAGCTTCTGACCTGACCTGACCTGACCTGACCTGACCTGAC 204
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QY 41 LeuThrIleThrTyrLeuLeuSerIleTyrPheGlyAsnLysTyrMetLysAsnAraPro 60
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DB 205 GTTACTGTCATGATCTCTCAATATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 264
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QY 61 AlaLeuSerLeuAlaGlyTyrIleLeuThrLeuTyrAsnLeuAlaIleThrLeuLeuSerAla 80
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DB 265 GCTATTCTCTCAGGGTATCTCAGCTGATTAATCTTGAATCATCATCTTCTCTCGGG 324
|||||

QY 81 TyrMetLeuValGluLeuIleLeuSerSerTyrPheGlyGlyTyrAsnLeuLeuLysGln 100
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DB 425 TACATGCTGACAGACATCTCTCCACTTGGCAGAGAGCTACAACTTACAGTGCA 384
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QY 101 AsnLeuAspSerAlaGlyGlyValAspValAlaValAlaLysValIleTyrTyrTyrTyr 120
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DB 495 GATCTTACAGGAGGAGAGAGCTGATCTGCGGTAGCAAGGTGTTTGGTGGTACTAT 444
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QY 121 PheSerLysLeuValGluPheLeuAspThrIlePhePheValLeuAlaGlyLysTyrAsn 140
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DB 445 TTCTCCAAATCAGTAGAATCTCTGACACAAATTTCTCTTTTGGGGAAAAAGAGCT 504
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QY 141 GlnIleThrPheLeuIleValTyrIleIleAlaSerMetPheAsnIleTyrTrpCysVal 160
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DB 505 CAGATATCTTCTTCATGATATATCATCATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 564
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QY 161 LeuAsnTrpIleProCysGlyGlnSerPhePheGlyProThrLeuAsnSerPheIleLeu 180
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DB 565 TTGAAGTGGATATCTTGGAGCAAAAGTTCTTTGGAGCAAACTGAAACATTTATTCAC 624
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QY 181 IleLeuMetTyrSerTyrTyrLeuSerValPheProSerMetHisLysTyrLeuTyr 200
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DB 625 ATTCTAATCTACTCTACTAATGAGCTTCTCTGTTTCAATCAATCAATCAATCAAT 684
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QY 201 TrpLysLysTyrLeuThrGlnAlaGlnLeuValIlePheValLeuSerIleThrHisThr 220
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DB 685 TCGAAGAAATATCTCAACAGGCTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 744
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QY 221 LeuSerAlaValValLysProCysSerCysLeuPhePheCysLysLeuIlePheGlnSer 240
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DB 745 ATGAAGAAATGCTGAAAGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 804
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QY 241 TyrMetMetThrLeuValIleLeuPheLeuAspThrIleThrLeuThrTyrAlaGlyLys 260
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DB 805 TATATGCTAAGCTTAGTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 864
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QY 261 ProValLysLysGluLeuGlnGlnLysValLysAsnGlyPhePro 276
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DB 865 CCAATGAAGAAGATATGCAAGAGCCATCTGACGAGGAAGCAAGCAAGCAAGCAAGCA 924
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QY 277 LysAlaHisLeuIleValAlaAsnGlyMetThrAspLysLysAlaGln 292
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DB 925 AAGGCTTACTTCACTGACGAGCAATGGAGTGAATGAAATGAAATGAAATGAAATG 972
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RESULT 4

ABV24286

DB ABV24286 standard: cDNA: 3645 BP.

XX AC ABV24286;

XX 16 SEP 2002 (first entry)

XX Human prostate expression marker cDNA 24277.

DE Human: prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;

XX KW pharmacogenomic marker; gene; ss.

XX KW Homo sapiens.

OS WO200160860 A2.

PN 23 AUG 2001.

FE 20 FEB 2003; 2901WG 0805171.

XX 17 FEB 2000; 2000US 18419P.

PR 16 MAR 2000; 2000US 189662P.

FE 25 MAY 2000; 2000US 207454P.

PR 09 JUN 2000; 2000US 211414P.

PR 18 JUN 2000; 2000US 219007P.

PR 14 DEC 2000; 2000US 255281P.

XX (MILL) MILLENNIUM PREDICTIVE MEDICINE INC.

PA Schlegel R, Endoqa WD, Mondhan JE;

XX WPI: 2001-662795/76.

XX Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer.

PS Claim 1; Page 4543 4544; 11750pp; English.

XX The invention relates to an isolated nucleic acid molecule (1) comprising a nucleotide sequence given in Tables 1-9 (ABV62213) of the specification or its complement. (1) is useful for:

CC (a) assessing whether a patient is afflicted with prostate cancer;

CC (b) monitoring the progression of prostate cancer in a patient;

CC (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;

CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;

CC (e) selecting a composition for inhibiting prostate cancer in a patient;

CC (l) assessing the prostate cell carcinogenic potential of a compound;
 CC (q) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.

XX
 SQ Sequence 3645 BP: 1041 A: 793 C: 684 G: 1119 T: 8 other:

Alignment Scores:

Prod. No.: 5,360-139 Length: 3645
 Score: 1431.00 Matches: 262
 Percent Similarity: 93.92% Conservative: 16
 Best Local Similarity: 88.51% Mismatches: 14
 Query Match: 91.32% Indels: 4
 DB: 23 Gaps: 1

US-09-624-670-63 (1-292) x ABV28431 (1-3645)

QY 1 MetGluGlnLeuLysAlaPheAspAsnGlnValAsnAlaPheLeuAspAsnMetPheGly 20
 DB 85 ATGGAACATCTAAAGGCTTCATCATCAATCAATGCTTTTGGACAAATGCTTGGGA 144
 QY 21 PheArgAspSerArgValArgGlyTyrPheLeuLeuAspSerTyrLeuProThrPheLe 40
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 QY 41 LeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLe 60
 DB 205 CTATCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 204
 QY 61 AlaLeuSerLeuArgGlyLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 80
 DB 265 GCTTTTCTCTCAGGGGATGCTCAGCTTGTATTAATCTTGGAAATACACTTCTCTGG 324
 QY 81 TyrMetLeuValGlnLeuLeuLeuSerSerTrpGlyGlyTyrAsnLeuGlnGlyGln 100
 DB 325 TACATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 384
 QY 101 AsnLeuAspSerAlaGlyGlyGlyAspValArgValAlaLysValLeuLeuTrpTyrTyr 120
 DB 385 GATCTTACCAGCGCAGCGCAGCGCAGCGCAGCGCAGCGCAGCGCAGCGCAGCGCAG 444
 QY 121 PheSerLysLeuValGlnPheLeuAspThrPhePheValLeuArgLysLysThrAsp 140
 DB 445 TTTCTCCAAATCAGTACAGTCTTGGACACAAATTTTCTCTTCTCTCTCTCTCTCT 504
 QY 141 GlnLeuLeuPheLeuHisValTyrHisHisAlaSerMetPheAsnLeuLeuTrpCysVal 160
 DB 505 CAGATTACTTTCT 554
 QY 161 LeuAsnTrpLeuProCysGlyCysSerPhePheGlyProPheLeuAsnSerPheLeHis 180
 DB 565 TGAACCTGATACCTTCT 624
 QY 181 TrpLeuMetTyrSerTyrTyrGlyGlySerValPheProSerMetHisLysTyrLeuTrp 200
 DB 625 ATTCTTATCTACT 684
 QY 201 TrpLysLysTyrLeuThrGlnAlaLeuLeuValGlnLeuValLeuThrHisThr 220
 DB 685 TGAACCTGATACCTTCT 744
 QY 221 LeuSerAlaValValLysProCysGlyPhePhePheGlyCysLeuLeuPheGlnSerSer 240
 DB 745 ATGAGGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 804
 QY 241 TyrMetMetThrLeuValLeuLeuPheLeuAsnPheTyrLeuGlnThrTrpArgLysLys 260
 DB 805 TATATGCTAACCTTACTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 864
 QY 261 ProValLysLysLeuLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 276
 DB 865 CTAAATGAGAAAT 924

QY 277 LysAlaHisLeuValValAlaAsnGlyMetThrAspLysLysAlaGln 292
 DB 925 AAAGGCTTACCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 972

RESULT 5

ABV28431
 ID ABV28431 standard: cDNA: 3645 BP.

XX AC ABV28431;

XX 16-SEP-2002 (first entry)

XX Human prostate expression marker cDNA 28422.

XX Human: prostate cancer, cytostatic, carcinogen, pharmacodynamic marker;
 KW pharmacogenomic marker, gene; ss.

XX OS Homo sapiens.

XX PN W0200150860-A2.

XX PD 23 AUG-2001.

XX PF 20-FEB-2001; 2001WG-US05171.

XX PK 17-FEB-2001; 2000US-183319P.

XX PP 16-MAR-2000; 2000US-189862P.

XX PP 25-MAY-2000; 2000US-207454P.

XX PP 09-JUN-2000; 2000US-211314P.

XX PP 18-JUL-2000; 2000US-219007P.

XX PP 13-DEC-2000; 2000US-255281P.

XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX PI Schlegel R, Endege WO, Monahan JE;

XX WPI: 2001-662795/76.

XX Claim 1: Page 5930-5931: 11750pp; English.

XX The invention relates to an isolated nucleic acid molecule (1) comprising a nucleotide sequence given in tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (1) is useful for:

CC (a) assessing whether a patient is afflicted with prostate cancer;

CC (b) monitoring the progression of prostate cancer in a patient;

CC (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;

CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;

CC (e) selecting a composition for inhibiting prostate cancer in a patient;

CC (f) assessing the prostate cell carcinogenic potential of a compound;

CC (g) determining whether prostate cancer has metastasized in a patient;

CC (h) assessing the aggressiveness or indolence of prostate cancer in a patient;

CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.

XX Sequence 3645 BP: 1041 A: 793 C: 684 G: 1119 T: 8 other:

Alignment Scores:

Prod. No.: 5,360-139 Length: 3645
 Score: 1431.00 Matches: 262
 Percent Similarity: 93.92% Conservative: 16
 Best Local Similarity: 88.51% Mismatches: 14
 Query Match: 91.32% Indels: 4
 DB: 23 Gaps: 1

US-09-624-670-63 (1-292) x ABV28431 (1-3645)

534 AAACATCATAGAAATTTATGAG/ACTTCTGCTTCATCTGCGAAGAACACACACAGATC 593
 143 ThrPheLeuHisValTyrHisHisAlaSerMetPheAsnIleThrPheCysValLeuAsn 162
 594 AGGTCCTGCAAGCTACACACATGCGCTGATGCTGAAATCATCTGGTGGTTTGTGATGAAC 653
 163 TrpIleProTyrGlyGluSerPhePheGlyProThrLeuAsnSerPheIleHisIleLeu 182
 654 TGGGTCCTCGCGGACACTCTATTTTGGTGGCCACACTTAATPACTTCAACACAGGCCCTC 713
 183 MetTyrSerTyrTyrGlyLeuSerValPhePheSerMetHisLysTyrLeuTrpTrpLys 202
 714 ATGTACTCTTACTATGATTTTGTGTCAGTCCATTCATGCTGTCATACCTCTGGTGGAG 773
 203 LysTyrLeuThrGlnAlaGlnLeuValGlnPheValLeuThrIleThrHisThrLeuSer 222
 774 AAGTACATCACTCAGGAGAACTGCTTCATTTGTGTGACAAATCATCCAGACCTGC 833
 223 AlaValValLysProGlyGlyPheProPheGlyCysLeuIlePheGlnSerSerTyrMet 242
 834 GGGGCAICAGCGCGCTGACATTCCTCTTCTGCTGCTGATTTCCAGATGGATACAC 893
 243 MetThrLeuValIleLeuPheLeuAsnPheTyrIleLeuThrTyrAlaLysLysProVal 262
 894 ATTTCCTGATGTCTCTTCACAAACTTCTATACATTCAGACCTACAAACAGAAAGGGGCG 953
 263 LysGlyGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 281
 954 TCCGAGAGAGAAAGACATTCAGGACACAGAAATGAGG-----TCCATGGAT 1001
 282 ValAlaAsnGlyMetThrAsp 288
 1002 GCTGTGAATGGACACACAAAC 1022
 RESULT 8
 ABV24778
 ID ABV24778 standard: cDNA; 2001 BP.
 AC ABV24778;
 DT 16-SEP-2002 (first entry)
 DE Human prostate expression marker cDNA 24769.
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss
 OS Homo sapiens.
 ON W0200160860 A2.
 XX 24 AUG-2001.
 XX 20 FEB-2001; 2001W010505171
 XX 17 FEB-2000; 2000US 184319P.
 XX 16 MAR 2000; 2000US 189862P.
 XX 25 MAY-2000; 2000US 207454P.
 XX 09-JUN-2000; 2000US 211314P.
 XX 18-JUL-2000; 2000US 219307P.
 XX 13 DEC-2000; 2000US 255281P.
 PA (MILL.) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX
 XX Schlegel R, Endege WJ, Monahan JE;
 XX WPI; 2001-662795/76.
 XX Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer
 XX

PS Claim 1; Page 4740-4741; 11750pp; English.

XX The invention relates to an isolated nucleic acid molecule (1) comprising
 CC a nucleotide sequence given in Tables 1-5 (AAGGAGGAG ARV62213) of the
 CC specification or its complement. (1) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (1) is also useful as a pharmacodynamic or pharmacogenomic marker.
 XX

Sequence 2001 BP; 527 A; 581 C; 399 G; 489 T; 5 other;

Alignment Scores:

Prod. No.: 2,650-89 Length: 2001
 Score: 951.50 Matches: 167
 Percent Similarity: 72.82% Conservations: 42
 Best Local Similarity: 58.19% Mismatches: 74
 Query Match: 69.72% Indels: 1
 DB: 23 Gaps: 2

US 09-624-670-63 (1 292) x ARV24778 (1 2001)

QY 3 GlnLeuLysAlaPheAspAsnGluValAsnAlaPheLeuAspAsnMetPheGlyProArg 22
 DB 174 CAATGGCAACATTTGATGCATCATCTAGTACCTATTTCAAGCATTCGTAAGGCTCGA 233
 QY 23 AspSerArgValArgGlyThrPheLeuLeuAspSerTyrLeuProThrIleLeuLeuThr 42
 DB 234 CATACCTAGCTAAAGAGATGTTCTTCTGAGCAATATATATACATTCATTTGCTCT 293
 QY 43 IleThrTyrLeuLeuSerIleThrPheGlyAsnLysTyrMetLysAsnArgProAlaLeu 62
 DB 294 GTCAATATTTTACATTTGATGCTGGCACTAAATACATACAGAAATAAAAGTCATTC 353
 QY 63 SerLeuArgGlyIleLeuThrLeuTyrAsnLeuAlaIleThrIleLeuSerAlaTyrMet 82
 DB 454 TCTTCTCTGGGAGATTTATTTGTTGTTATTAATCTTGGACATTCATCTGTTCTGATATG 413
 QY 83 LeuValGlnLeuIleLeuSerSerTyrGlyGlyGlyTyrAsnLeuLeuGlySerIleLeu 102
 DB 414 TTCTGTGAGTTAGTACAGAGCTATGGAGAGCAATAACAAATTTTGTGTAGGGACCA 473
 QY 103 AspSerAlaGlyGlyGlyAspValArgValAlaLysValLeuThrPheTyrTrpPheSer 122
 DB 474 GGCAGCGAGCAGAAATCAGATATGAAATATTCGCTGCTGCTGCTGCTGCTGCTGCTGCT 533
 QY 123 LysLeuValGlnPheLeuAspThrIlePhePheValLeuArgGlyLysThrAsnGlnIleP 142
 DB 534 AAACCTATAGAAATTTATGGACACTTCTCTTCTATGCTTCTGGAGAAACAAACACAGATC 593
 QY 143 ThrPheLeuHisValTyrHisHisAlaSerMetPheAsnIleThrPheCysValLeuAsn 162
 DB 594 AGGTCCTGCAAGCTACACACATGCGCTGATGCTGAAATCATCTGGTGGTTTGTGATGAAC 653
 QY 163 TrpIleProTyrGlyGluSerPhePheGlyProThrLeuAsnSerPheIleHisIleLeu 182
 DB 654 TGGGTCCTCGCGGACACTCTATTTTGGTGGCCACACTTAATPACTTCAACACAGGCCCTC 713
 QY 183 MetTyrSerTyrTyrGlyLeuSerValPhePheSerMetHisLysTyrLeuTrpTrpLys 202
 DB 714 ATGTACTCTTACTATGATTTTGTGTCAGTCCATTCATGCTGTCATACCTCTGGTGGAG 773
 QY 203 LysTyrLeuThrGlnAlaGlnLeuValGlnPheValLeuThrIleThrHisThrLeuSer 222
 DB 774 AAGTACATCACTCAGGAGAACTGCTTCATTTGTGTGACAAATCATCCAGACCTGC 833

OY	223	AAlaValIValLysPheGlyCysGlyPheThrPheGlyGlySerLeuTcPheCHisSerSerTyMet	242
Dbb	834	GAGATATTACGGCGGTGAATACTCATTTTGTTGTTTATTTCATAATTGATATGCATG	893
OY	243	MctThrLeuValILeuleuPheLeuAsnPhetTrLLcGluThrTYtArgLylysProVal	262
Ddb	894	ATFTCCCTGATGCTCTCTCTCAACAACACTCTCACATTCAGACTACAAACAAGAAGGCC	953
OY	263	LysLysGluLeuGlnGlu---LysGluValLysAsnGlyPheProLysAlaHIsLeuIle	281
Ddb	954	TCCCAGAACAAAATCAAATCTGAAGAGCAACACAAATGGG-----TCCATGGCT	1001
OY	282	ValAlaAsnGlyMethThrAsp	288
Ddb	1002	GTCTGTGAATGGATACATTAAC	1022
RESULT 9			
ABV25364			
ID	ABV25364	standard; cDNA; 2001 BP.	
XX	AC	ABV25364;	
XX	CC		
XX	DT	16-SEP-2002 (first entry)	
XX	DD	Human prostate expression marker cdNA 25355.	
DE	DE		
KW	KW	Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;	
KW	KW	pharmacogenic marker; gene; ss.	
OS	OS	Homo sapiens.	
XX	WO	2000150R60-A2	
XX	PD	23-ASG 2001.	
PP	PP	20-FEB-2001; 2001WO-US05171.	
XX	PP	17-FER-2000; 2000US-183319P.	
PP	PP	16-MAR-2000; 2000US-189862P.	
PP	PP	25-MAY-2000; 2000US-207454F.	
PP	PP	09-JUN-2000; 2000US-211314P.	
PP	PP	18-JUL-2000; 2000US-219007P.	
PP	PP	13-DEC-2000; 2000US-255281P.	
XX	(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.		
PA	Schlegel R, Endege WO, Monahan JE;		
XX	WPI; 2001-662795/76.		
PT	Novel isolated nucleic acid molecule associated with cancerous state of		
PT	prostate cells and correlating with presence of prostate cancer, useful		
PT	for detecting presence of prostate cancer, stage of prostate cancer -		
PS	Claim 1; Page 5005-5006; 11750pp; English.		
XX	The invention relates to an isolated nucleic acid molecule (I) comprising		
CC	a nucleotide sequence given in Tables 1 & 2 (Assessing Nucleic Acids) of the		
CC	specification or its complement. (II) is useful for:		
CC	(a) assessing whether a patient is afflicted with prostate cancer,		
CC	(b) monitoring the progression of prostate cancer in a patient;		
CC	(c) assessing the efficacy of a test compound to inhibit prostate		
CC	cancer in a patient;		
CC	(d) assessing the efficacy of a therapy for inhibiting prostate cancer		
CC	in a patient;		
CC	(e) selecting a composition for inhibiting prostate cancer in a patient;		
CC	(f) assessing the prostate cell carcinogenic potential of a compound;		
CC	(g) determining whether prostate cancer has metastasized in a patient;		
CC	(h) assessing the aggressiveness or indolence of prostate cancer in a		
CC	patient;		
CC	(I) is also useful as a pharmacodynamic or pharmacogenomic marker.		

Mon Jun 16 09:01:12 2003

OS Homo sapiens.
 PN W0200660082-A2
 XX
 PD 12-07T-2000
 XX
 PP 06-APR-2000; 2000W0-US09353.
 XX
 PR 07-APR-1999; 9908-0128193.
 PR 20-JUL-1999; 9908-0144701.
 XX
 PA (INCY-) INCYTE PHARM INC.
 XX
 PI Lai P, Yue H, Hillman JI., Baughn MR, Tang YT, Lu DAM, Azimzai Y;
 DR WPI: 2000-665006/64.
 DR P-PSDB: AAB24240.
 XX
 PT New vesicle associated proteins (VRAS) and polynucleotides encoding
 PT VRAS for diagnosing, treating or preventing transport disorders (e.g.
 PT Bell's palsy), autoimmune/inflammatory disorders (e.g. AIDS) or cancer
 PT (e.g. leukemia)
 XX
 PS Claim 4; page 111:112; 112pp: English.
 XX
 CC AAC60985 to AAC61000 and AAC64367 to AAC64369 encode the human vesicle
 CC associated proteins 1 to 19 (VEAS-1 to 19) given in AAB24222 to AAB24240.
 CC Human VEAS proteins have nontoxic, immunosuppressive, antibacterial,
 CC fungicide, antihelminthic, protozoacide, virucide, anti-inflammatory and
 CC cytostatic activities. The isolated polypeptides and polynucleotides are
 CC useful for diagnosing, treating or preventing transport disorders (e.g.
 CC akinesia, Bell's palsy, diabetes mellitus, catatonia, infectious
 CC myositis, dementia, Grave's disease or AIDS), autoimmune/inflammatory
 CC disorders (e.g. AIDS, asthma, bronchitis, Ketter's syndrome, systemic
 CC lupus erythematosus, rheumatoid arthritis, or viral, fungal, bacterial,
 CC protozoal or helminthic infections), or cancer (e.g. adenocarcinoma,
 CC leukemia, melanoma, sarcoma, or gall bladder, heart, kidney, bone,
 CC brain, breast, pancreas or skin cancers). The polypeptides may also be
 CC used to immunise a host animal. The polypeptides and polynucleotides are
 CC further useful for screening libraries of compounds or for drug
 CC screening assays.
 XX
 SQ Sequence 2313 BP; 645 A; 486 C; 480 G; 702 T; 0 other;
 Alignment Scores:
 Pred. No.: 3, 23e-89 Length: 2313
 Score: 951.50 Matches: 167
 Percent Similarity: 72.82% Conservative: 42
 Host/Local Similarity: 58.39% Mismatches: 73
 Query Match: 50.72% Indels: 5
 DB: 21 Gaps: 2
 US-09-624-670-63 (1-292) x AM64369 (1-2313)
 QY 3 GlnLeuLysAlaPheAspAsnGluValAsnAlaPheLeuAspAsnMetPheGlyProArg 22
 DB 161 CAATGGGAACATTTTGGATGATACATCTAGTACCTATTTCAGGCATTTGTAGCCCTCGA 220
 QY 23 AspSerArgValArgGlyTrpPheLeuLeuAspSerTyrLeuProThrPheLeuThr 42
 DB 221 GATACATAGAGTAAAGAGATGTTCTTCTGGACAAATATATACCCACATTTATCTGCTCT 280
 QY 43 IleThrTyrLeuLeuSerIleTrpLeuGlyAsnLysTyrMetLysAsnArgProAlaLeu 62
 DB 281 GTCATATATTTACTAATTTGTATGGCTGGACAAATACATAGGAAATAAACAGCCATTC 340
 QY 63 SerLeuArgGlyIleLeuThrLeuTyrAsnLeuAlaIleThrLeuLeuSerAlaTyrMet 82
 DB 341 TCTTGGCGGGGATTTTGTAGTGTATACCTTGGACTTCACACTGCTGCTCTGTATATG 400
 QY 83 LeuValGluLeuLeuSerSerTrpGluIleGlyTyrAsnLeuGlnCysGlnAsnLeu 102
 DB 401 TTCTGTGAGTTAGTAAACAGCAGTATGGGAAGCAAAATACAACTTCTTCTGTCAGGCACA 460
 QY 103 AspSerAlaGlyGluGlyAspValArgValAlaLysValLeuTrpTyrTyrPheSer 122
 DB 461 CGCACGACAGAGATCATGATATGAAGATTTATCCGCTGCTCTGCTGATACCTTCTCC 520
 QY 123 LysLeuValGluPheLeuAspThrIlePhePheValLeuArgLysLysThrAsnGlnIle 142
 DB 521 AAACATCATAGATTTTATGGACACTTTCTTCTCATCTGCTGCAAGAAACAACACCATC 580
 QY 143 ThrPheLeuHisValTyrHisAlaSerMetPheAsnIleTrpTrpCysValLeuAsn 162
 DB 581 ACGGTCTGTCACGCTACCAACCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 640
 QY 163 TrpIleProCysGlyGlnSerPhePheGlyProThrLeuAsnSerPheIleHisLeu 182
 DB 641 TGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 700
 QY 183 MetTyrSerTyrTyrGlyLeuSerValPheProSerMetHisLysTyrLeuTrpTrp 202
 DB 701 ATGTACTTCTTACTATGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 760
 QY 203 LysTyrLeuThrGlnAlaGlnLeuValGlnPheValLeuThrIleThrHisThrLeuSer 222
 DB 761 AACTACATCACTCAGGGGAGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 820
 QY 223 AlaValLysProCysGlyPhePheGlyCysLeuIlePheGlnSerSerTyrMet 242
 DB 821 GGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 880
 QY 243 MetThrLeuValIleLeuPheLeuAsnPheThrIleGlnThrTyrArgLysLysProVal 262
 DB 881 ATCTCCCTGATGCTCTCTTCTTCAAACTTCTTCACTTACATTCAGACCTTCAACAAGAGGGGCC 940
 QY 263 LysLysGluLeuGlnGlu---LysGluValLysGlnPheProLysAlaHisLeuIle 281
 DB 941 TCCCAAGAAAGAACCACTGAGGACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 988
 QY 282 ValAlaAsnGlyMetThrAsp 288
 DB 989 GCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1009
 RESULT 12
 AAK94320
 ID AAK94320 standard; cDNA: 2627 BP.
 XX
 AC AAK94320:
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human full-length cDNA, SEQ ID NO: 2997.
 XX
 KW Human; full length cDNA: cDNA synthesis; oligo-capping; ss.
 XX
 OS Homo sapiens.
 XX
 PN EP1130054-A2.
 XX
 PD 05-SEP-2001.
 XX
 PP 07-JUL-2000; 2000EP-0114089
 XX
 PR 08-JUL-1999; 99JF-0194486.
 PR 11-JAN-2000; 2000JF-0118774.
 PR 02-MAY-2000; 2000JF-0183765.
 XX
 PA (HELI-) HELIX RES INST.
 XX
 PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
 PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
 XX
 DR WPI: 2001-524255/58.
 DR P-PSDB: AAN93399.
 XX

CC such as leukaemia, lymphoma and neuroblastoma, autoimmune disorders such
 CC as multiple sclerosis, connective tissue disease, rheumatoid arthritis,
 CC diabetes mellitus, allergic rhinitis, asthma and eczema, nervous system
 CC disorders such as Parkinson's disease, Alzheimer's disease, Huntington's
 CC chorea, amyotrophic lateral sclerosis, spinal muscular atrophy and
 CC Wernicke disease, inflammatory disorders such as nephritis, Crohn's
 CC disease, ischaemia reperfusion injury, shock, sepsis and inflammatory
 CC bowel disease. The sequences exhibit activity relating to angiogenesis,
 CC cell proliferation, cell differentiation, stem cell growth factor,
 CC activin or inhibin. Therefore, they can be used to manipulate stem cells
 CC in culture to give rise to neuroepithelial cells that can be used to
 CC augment or replace cells damaged by illness, accidental damage or genetic
 CC disorders. The sequences may also be used for regeneration of bone,
 CC cartilage, tendons and ligaments and in tissue repair and burn healing.
 CC Note: Some sequences for this patent did not form part of the printed
 CC specification, but were obtained in electronic format directly from WIPO
 CC at http://wipo.int/pub/published_pat_sequences.

xx Sequence 2769 BP; 799 A; 543 C; 554 G; 873 T; 0 other;

Alignment Scores:

Field No.: 4,13e-89 Length: 2769
 Score: 951.50 Matches: 167
 Percent Similarity: 72.82% Conservativ: 42
 Best Local Similarity: 58.19% Mismatches: 73
 Query Match: 60.72% Indels: 5
 DB: 22 Gaps: 2

US-09-624-670-63 (1-292) x AAS44747 (1-2769)

QY 3 GlnLeuLysAlaPheAspAsnGluValAlaAsnAlaPheLeuAspAsnMetPheGlyProArg 22
 Db 133 CAATGGACATTTTGTATGATCATCATCTTATGACCTATTTCAAGCATGCTAGGCCCCGCA 192
 QY 23 AspSerArgValArgGlyTrpPheLeuLeuAspSerTrpLeuProThrPheIleLeuThr 42
 Db 193 GATACTAGAGTAAAGCATCGTTCTTCTGCGACATATATACCCACATTTATCTGCTCT 252
 QY 43 IleThrTyrLeuLeuSerIleTrpLeuGlyAsnLysTyrMetLysAsnArgProAlaLeu 62
 Db 253 GTCAATATTTTCAATATGATGCTGGAGCAAAATAATATGAGGAATAAACAGCCATTC 312
 QY 63 SerLeuArgGlyIleLeuThrTrpLeuTyrAsnLeuAlaIleThrLeuLeuSerAlaTyrMet 82
 Db 313 TCTTGCGAGGAGGATTTTATGATGATATAAAATTGATATCTCTCTCTCTATATG 372
 QY 83 LeuValGluLeuIleLeuSerTrpTrpGlyGlyTyrAsnLeuGlnGlyGlnAsnLeu 102
 Db 373 TTCGTCGACATTAACAAATAGATAGGGAAGGCAAAATACAACTTCTCTGCAAGGACAA 432
 QY 103 AspSerAlaGlyGlyGlyAspValArgValAlaLysValLeuTrpTrpTyrTyrPheSer 122
 Db 433 CGAACGGAGAGAAAT 492
 QY 123 LysLeuValGluPheLeuAspThrIleIlePheValLeuArgLysLysThrAsnGlnIle 142
 Db 493 AAACATCATGAAATTAAGAGAAATTTTCTTCTTCTATATATATATATATATATATAT 552
 QY 143 ThrPheLeuHisValTrpTrpHisAlaSerMetPheAsnIleTrpTrpCysValLeuAsn 162
 Db 553 ACGGTCCTGATGAGGAGAAATATATATATATATATATATATATATATATATATATAT 612
 QY 163 TrpIleProCysGlyGlnSerPheGlyProThrLeuAsnSerPheIleHisLeu 182
 Db 613 TGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 672
 QY 183 MetTyrSerTyrTyrGlyLeuSerValPheProSerMetHisLysTyrLeuTrpTrpLys 202
 Db 673 ATGATATTTAT 732
 QY 203 LysTyrLeuThrGlnAlaGlnValGlnPheValIleThrIleThrHisThrLeuSer 222
 Db 733 AACTATACATACATACATACATACATACATACATACATACATACATACATACATACAT 792

QY 223 AlaValValLysProCysGlyPheProPheGlyCysLeuIlePheGlnSerSerTyrMet 242
 Db 793 GGGATCACTGGCGGCGACCAATTCCTCTTGGTTGGTTGTTATTCAGATTGGATCATG 852
 QY 243 MetThrLeuValIleLeuPheLeuAsnPheTyrIleGlnThrTyrArgLysLysProVal 262
 Db 853 ATTCCCTGATGTGCTCTCTTCAAACTTCTACATTCAGACTCAACAAGAAAGGGGCC 912
 QY 263 LysLysGluLeuGlnGlu---LysGluValLysAsnGlyPheProLysAlaHisLeuIle 281
 Db 913 TCCCAGAGGAAAGACCACTCAAGGACCACCAAGATGG-----TCCATGGCT 960
 QY 282 ValAlaAsnGlyMetThrAsp 288
 Db 961 GGTGTATATGAGACACACCAAC 981

RESULT 14

AAS44919
 ID AAS44919 standard; DNA; 3083 BP.

AC AAS44919;

XX 18-DEC-2001 (first entry)

DE Human contig polynucleotide sequence #172.

XX Mammal; human; rhesus monkey; baker's yeast; fission yeast; Norway rat;

XX mouse; Chinese hamster, African clawed frog, fruit fly, dog; leukaemia;

XX cancer; lymphoma; neuroblastoma; autoimmune disorder; cell proliferation;

XX nervous system disorder; inflammatory disorder; cell differentiation; ds;

XX angiogenesis; stem cell growth factor; activin; inhibin; cartilage; burn;

XX genetic disorder; bone regeneration; tendon; ligament; tissue repair;

XX cytostatic; antirheumatic; antiarthritic; vulnery; antinflammatory;

XX antibacterial; immunosuppressive; vasotrophic; antiparkinsonian;

XX neuroprotective; osteopathic; antidiabetic; antiaesthetic; antiallergic;

XX immunostimulant; analgesic; gene therapy.

OS Homo sapiens.

OS Synthetic.

XX WO200164834-A2.

XX 07-SEP-2001.

XX 26-FEB-2001; 2001WO-0504926.

XX 28-FEB-2000; 2000US-0515126.

XX 18-MAY-2000; 2000US-0577409.

XX 17-JUN-2000; 2000US-0597707.

XX 14-JUL-2000; 2000US-0615807.

XX 19-SEP-2000; 2000US-0664641.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;

XX Xue AJ, Yang Y, Wehrman T, Wang J, Ma Y, Wang D, Chen R, Xu C;

XX Drmanac R;

XX WPI: 2001-589862/66.

XX P-PSDB: AAS28019.

XX Novel polypeptides and nucleic acids obtained from cDNA libraries

XX prepared from various human tissues, for diagnosis, treatment of

XX cancer, neurological, inflammatory disorders and for use in arrays for

XX detection -

XX Claim 1: SEQ ID No 516; 153pp; English.

XX Sequences AAS44576-AAS44919 represent full-length polynucleotides and

XX contig polynucleotides encoding polypeptides of the invention. The DNA

XX and protein sequences are useful for the treatment, diagnosis and

XX prevention of various types of disorder in a mammalian subject such as a

Genome version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: June 15, 2003, 21:38:16 ; Search time 54 sec0.48 sec0.38
(without alignments)
1678.203 Million cell updates/sec

Title: US-09-624-670-63

Perfect score: 1567

Sequence: 1 MEOALAFNEVNAFLDNMF

Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 682724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

MODEL-frame.p2n.model -DEV-xip
O-/cgn2_1/USPTO.spool/USC96267/runat_11062003_075431_11654/app-query.fasta_1.910
DB-issued_patents_NA -QFMT-fastlap -SUFFIX-rnl -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS-bits -START=1 -END=1 -MATRIX-Blosum62 -TRANS-human40.cdi
-LIST=45 -DOCALLIGN=200 -THR_SCORE=pcl -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE-LOCAL -OUTFMT-pto -NORM-ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USRR-US09624670.cgn2_1.1.84.arunat_11062003_075431_11654 -NCPU=6 -ICPU=3
-NO_MMAP -IARGHOURRY -NIG.SCORER=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV-TIMEOUT=120 -WARN-TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database:

Issued_patents_NA:
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2: /cgn2_6/prodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/prodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/prodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/prodata/1/ina/PTTS.COMB.seq:*
6: /cgn2_6/prodata/1/ina/Backlist.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	462.5	29.5	1482	4	US-09-149-476-258
2	462.5	29.5	1542	4	US-09-149-476-106
3	292	18.6	1854	1	US-08-249-420-1
4	292	18.6	1854	2	US-08-737-663-1
5	279	17.8	954	4	US-09-145-828A-1
6	235	15.0	587	4	US-09-145-828A-9
7	232	14.8	590	4	US-09-145-828A-10
8	193	12.3	989	1	US-07-885-970A-7
9	193	12.3	989	1	US-08-298-687A-7
10	193	12.3	989	1	US-08-530-797-6
11	193	12.3	989	1	US-08-298-829-7
12	193	12.3	989	2	US-08-787-335-6

13	132	8.4	834	4	US-09-149-476-258
14	121	7.7	124	4	US-09-172-108-45
15	100	6.4	2310	1	US-08-417-330A-15
16	99.5	6.3	2051	1	US-08-672-814D-1
17	99.5	6.3	2051	4	US-08-333-696-1
18	97.5	6.2	1844	4	US-08-592-116-90
19	97	6.2	1236	4	US-08-887-534A-79
20	96	6.0	1272	4	US-09-134-001C-2373
21	94.5	6.0	4011	1	US-08-121-057-3
22	94.5	6.0	4011	2	US-08-509-187D-3
23	94.5	6.0	4011	1	US-09-121-396-3
24	94.5	6.0	4011	5	PCT-IN943-09704A-3
25	94.5	6.0	4079	1	US-08-121-057-2
26	94.5	6.0	4079	2	US-08-509-187D-3
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29	93.5	5.9	98843	4	US-09-791-211-10
30	93	5.9	2835	4	US-09-134-001C-1515
31	93	5.9	3561	4	US-09-134-001C-1685
32	93	5.9	6414	4	US-09-134-001C-1526
33	88	5.6	1714	3	US-08-961-083-3
34	88	5.6	2555	2	US-08-693-457-3
35	88	5.6	2555	4	US-09-265-731-3
36	88	5.6	1542	4	US-08-942-527-26
37	87.5	5.6	1430	2	US-08-179-557-15
38	87	5.6	6201	2	US-08-790-912-1
39	87	5.6	81001	4	US-09-750-580-1
40	86.5	5.5	1965	4	US-09-311-626B-13
41	85.5	5.5	1538	1	US-08-417-330A-13
42	85.5	5.5	2191	1	US-08-417-330A-11
43	85	5.4	1809	4	US-09-134-001C-1579
44	85	5.4	3807	2	US-08-823-001A-8
45	85	5.4	3807	4	US-08-642-2741-8

ALIGNMENTS

RESULT 1
US-09-149-476-258
Sequence 258, Application US/09149476
Patent No. 6420526
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human secreted proteins
FILE REFERENCE: P2002P1
CURRENT APPLICATION NUMBER: US/09/149,476
EARLIER FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/038,621
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,626
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,334
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,346
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,163
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/047,600
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,615
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,597
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,502
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,633
EARLIER FILING DATE: 1997-05-23

[illegible]

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1 EARLIER APPLICATION NUMBER: 60/0756, 875
2 EARLIER FILING DATE: 1997-08-22
3 EARLIER APPLICATION NUMBER: 60/0756, 882
4 EARLIER FILING DATE: 1997-08-22
5 EARLIER APPLICATION NUMBER: 60/0756, 887
6 EARLIER FILING DATE: 1997-08-22
7 EARLIER APPLICATION NUMBER: 60/0756, 908
8 EARLIER FILING DATE: 1997-08-22
9 EARLIER APPLICATION NUMBER: 60/0748, 964
10 EARLIER FILING DATE: 1997-05-06
11 EARLIER APPLICATION NUMBER: 60/0757, 650
12 EARLIER FILING DATE: 1997-09-05
13 EARLIER APPLICATION NUMBER: 60/0756, 884
14 EARLIER FILING DATE: 1997-08-22
15 EARLIER APPLICATION NUMBER: 60/0757, 669
16 EARLIER FILING DATE: 1997-09-05
17 EARLIER APPLICATION NUMBER: 60/0749, 610
18 EARLIER FILING DATE: 1997-06-13
19 EARLIER APPLICATION NUMBER: 60/0761, 960
20 EARLIER FILING DATE: 1997-10-02

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EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047, 598
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047, 613
EARLIER FILING DATE:	1997-05-23
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EARLIER APPLICATION NUMBER:	60/047, 596
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047, 612
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047, 632
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047, 601
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/043, 580
EARLIER FILING DATE:	1997-04-11
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EARLIER APPLICATION NUMBER:	60/043, 569
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EARLIER APPLICATION NUMBER:	60/043, 311
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EARLIER APPLICATION NUMBER:	60/043, 674
EARLIER FILING DATE:	1997-04-11
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EARLIER FILING DATE:	1997-04-11
EARLIER APPLICATION NUMBER:	60/043, 412
EARLIER FILING DATE:	1997-04-11
EARLIER APPLICATION NUMBER:	60/043, 313
EARLIER FILING DATE:	1997-04-11
EARLIER APPLICATION NUMBER:	60/043, 672
EARLIER FILING DATE:	1997-04-11
EARLIER APPLICATION NUMBER:	60/043, 315
EARLIER FILING DATE:	1997-04-11
EARLIER APPLICATION NUMBER:	60/048, 974
EARLIER FILING DATE:	1997-06-06
EARLIER APPLICATION NUMBER:	60/056, 886
EARLIER FILING DATE:	1997-08-22
EARLIER APPLICATION NUMBER:	60/056, 877
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EARLIER APPLICATION NUMBER:	60/056, 889
EARLIER FILING DATE:	1997-08-22
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EARLIER APPLICATION NUMBER:	60/056, 662
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EARLIER APPLICATION NUMBER:	60/056, 872
EARLIER FILING DATE:	1997-08-22
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EARLIER APPLICATION NUMBER:	60/056, 888
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EARLIER APPLICATION NUMBER:	60/056, 894
EARLIER FILING DATE:	1997-08-22
EARLIER APPLICATION NUMBER:	60/056, 911
EARLIER FILING DATE:	1997-08-22

QY 234 Cysleuilephecinsertserlyrmetmetthruvalilleuupheleuasphetyr 253
DB 1447 TGGCCCATATTT---TCTTCATATTTG-----GTACTATTATTATTCATTAC 1491
QY 254 Ileglnthryrqrlyslspsrovallyslsghleuglnglulysgluvallylsasn 273
DB 1492 ATTAACGTTTATTAAGGTAAAGGACCAAAACAGTAGAGTGGTAAAGCGTCCCAAGCG 1551
QY 274 G1Y 274
DB 1552 GGT 1554

RESULT 5

US-09-145-828A-1
Sequence 1, Application US/09145828A
Patent No. 6403349
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pradip
APPLICANT: Leonard, Amanda E. Y.
APPLICANT: Huang, Yung-Sheng
APPLICANT: Thurmond, Jennifer
APPLICANT: Kitchner, Stephen J.
APPLICANT: Parker-Barnes, Jennifer M.
TITLE OF INVENTION: THE ELONGASE GENE AND USES THEREOF
FILE REFERENCE: 6407.LS.O1
CURRENT APPLICATION NUMBER: US/09/145,828A
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 954
TYPE: DNA
ORGANISM: Mortierella alpina
US-09-145-828A-1

Alignment Scores:

Pred. No.: 1 Re-23 Length: 264
Score: 279.00 Matches: 89
Percent Similarity: 42.99% Conservative: 55
Best Local Similarity: 26.57% Mismatches: 107
Query Match: 17.80% Indels: 84
DB: 4 Gaps: 13

US-09-624-670-63 (1-292) x US-09-145-828A-1 (1-954)

QY 9 AsnGluValAsnAlaPheLeuAspAsnMetPheGlyProAlaGAspSerAlaValArgly 28
DB 19 GACAAGGTCAACTCGCATTTGATGACGCTTGGATCAAG----- 60
QY 29 TrpPheLeuAspSerlyr-----Leu 36
DB 61 -----CTGCAGACCTACTTCTGCTAAAGTATGAATTTATATGGAAAGTCCAGC 111
QY 37 ProthpPheLeu----- 41
DB 112 GACTCTCTGCTTCCAGAGAGGAGTCAAGGCTCTCTGCAAGTAAAGAGAAAGTCTGAG 171
QY 42 ---ThrlleThrTyrlleuSerlleIlePleuGlyAsnLyslyrMetLysAsnArgPro 60
DB 172 TGCACATCACTTACTCTGCTGATTTGTTGTTGTCAGATATATATATATATATATATAT 231
QY 61 AlaLeuSerleuArgGlylleuThrleuThrleuThrleuThrleuThrleuThrleuThrleu 80
DB 232 GCGCTCAAGTCAAGTCT 291
QY 81 TyrMetLeuValGluLeuIle-----LeuSerSerTrpGlnGlylyr 95
DB 292 TCGCTGCT 351
QY 96 AsnLeuGlnGlyGlnAsnLeuAspSerAlaGlyGluGlyAspValArgValAlaLysVal 115

DB 352 TAGCATATTTGAGAGAG-----AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 399
QY 116 LeuIleTrpTyrlleTherSerlyslsleuValIlePheLeuAspPheIlePhePheValIleu 135
DB 400 TACTATCTTAATTAATCTCTCTCAAGTACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 459
QY 136 ArgLysLysThrAsnGlnIleThrPheLeuIleValIleHisLysAlaSerMetPheAsn 155
DB 460 AAGATATAT-----CT 513
QY 156 IleTrpTrpCysValIleu-----AsnTrpIleProCysGlyCysSer 169
DB 514 CTCTGTTTCTTCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 564
QY 170 PhePheGlyProThrLeuAsnSerPheIleHisIleLeuMetTyrlleTyrlleu 189
DB 565 -----AACCCCAACCTCAAGCTGACGCTGACGCTGACGCTGACGCTGACGCTGACGCT 612
QY 190 SerValPheProSerMetHisLysTyrlleuTrpTrpLysLysTyrlleGluAlaGln 209
DB 613 TCT-----CT 663
QY 210 LeuValClnPheValLeuThrIle-----ThrHisThrLeuSerAla 223
DB 664 ATGCTCGAGTCT 723
QY 224 Val-----ValLysProCysGlyPheProPheCysLys 235
DB 724 TTGACATCT 783
QY 236 IlePheGlnSerSerlyrMetMetThrLeuValIleLeuPheLeuAspPheTyrlleGln 255
DB 784 CTCTTCT 843
QY 256 ThrTyrlleGlyLysProValLysLysLysLysLysLysLysLysLysLysLysLysLys 275
DB 844 ACCTATAT-----GAG 894
QY 276 TrpGlyAlaHisIleClnIleValAlaAsnGlyMetClnAspArgLys 290
DB 895 CCGCAAGACT-----CTCAAGTCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 940

RESULT 6
US-09-145-828A-9
Sequence 9, Application US/09145828A
Patent No. 6403349
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pradip
APPLICANT: Leonard, Amanda E. Y.
APPLICANT: Huang, Yung-Sheng
APPLICANT: Thurmond, Jennifer
APPLICANT: Kitchner, Stephen J.
APPLICANT: Parker-Barnes, Jennifer M.
TITLE OF INVENTION: THE ELONGASE GENE AND USES THEREOF
FILE REFERENCE: 6407.US.O1
CURRENT APPLICATION NUMBER: US/09/145,828A
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9
LENGTH: 587
TYPE: DNA
ORGANISM: Mortierella alpina
US-09-145-828A-9

Alignment Scores:
Pred. No.: 1 29e-18 Length: 587
Score: 235.30 Matches: 62
Percent Similarity: 48.04% Conservative: 36
Best Local Similarity: 30.39% Mismatches: 68
Query Match: 15.00% Indels: 38
DB: 4 Gaps: 7

APPLICATION NUMBER: US/07/885,970A
FILING DATE: 19920518
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/617,239
FILING DATE: 21-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/253,243
FILING DATE: 04-OC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,386
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 233-2478
TELEFAX: (608) 251-5139
INFORMATION FOR SEQ. ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 989 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Gossypium hirsutum
STRAIN: Coker 312
DEVELOPMENTAL STAGE: 10 day old fiber cells
TISSUE TYPE: fiber cells
IMMEDIATE SOURCE:
LIBRARY: CKEB10
CLONE: A11
US-07-885-970A-7

Alignment Scores:
Pred. No.: 2.42e-13 Length: 989
Score: 193.00 Matches: 55
Percent Similarity: 44.55% Conservative: 35
Best Local Similarity: 27.23% Mismatches: 58
Query Match: 12.32% Indels: 54
Gaps: 10

US-09-624-670-63 (1-292) x US-07-885-970A-7 (1-989)

OY 115 ValLeuThrPrp-----TyrTyrPheSerLysLeuValGluPheLeuAspThrIle 131
Db 907 CTCTTTTCTGGGCAATACATCTTCTACCTCTCCACAGATTCTTAATTATACGACACCTCT 848
OY 132 PhePheValPheArqLysLysThrAsnGlnIleThrPheLeuHisValTyrHisHisAla 151
Db 847 TTGATCATCTCAACCGAATCCAGATCAAGACGCAATCCCTTCACCTCAACATCAACATCC 788
OY 152 SerMetPheAsnIleThrPrpCysValLeuAsnTrpIleProCysLysGlnSerPhePhe 171
Db 787 ATGATGATATCATATGATATATTATGATTAAG-----AGTGTCTAGTCTCCGTA 737
OY 172 GlyProThrLeu-----AsnSerPheIleHisIleLeuMetTyrSerTyrTyrGlyLeu 189
Db 736 CCCATGCTCTCAATCAACCACTCCCTGTCACATGCTGTAATGATACCTAATTAACCTG 677
OY 190 SerValPheProSerMetHisLysTyrLeuTrpTrpLysLysTyrLeuThrGlnAlaGln 209
Db 676 TGCACCGCTG---GGGATGCGACCCCAAG-----TGSAAACAAATGTCGCGATTTTCGA 626
OY 210 LeuValGlnPhe-----ValLeuThrIleThrHisThrLeu 221
Db 625 CTGATGAGTTCGCGTAAAGCTTTTGATCATGCGCATGATGATGATGATTAATTAAT 566
OY 222 SerAlaValAlaLysProCysGlyPheProPheGlyCys-----LeuIle 236
Db 565 GCTTCT-----GCTGCTGCTGCGCATTCGCTGCTGCTGCT 533
OY 237 PheInserSerTyrMetMetThrLeuValIleLeuPheLeuAsnPheTyrIleGlnThr 256

Db 532 ITCAATGAGCTTTCAACATCTCTCTCTATCTTCTTCAATTTCAATTTCAATGAGGT 473
OY 257 TYTATGlySerProValLysGlySerLeuGlnGlyGlnValLysAsn 273
Db 472 TAT-----TCCATGATGCGAATGCTTCAATGCTTCAATGCTTCAATGCTTCAAT 434
OY 274 -----GlyPheProGlnAlaHisLeuIleVal 282
Db 433 TTAATTAACCAACTTTTTTGTGTTTTCCATTTGCTTTCCATGCTTCAATGCTTCAAT 374
OY 283 AlaAsn 284
Db 373 GTTCA 368

RESULT 9
US-08-298-687A-7/c
Sequence 7, Application US/08298687A
Patent No. 5521078
GENERAL INFORMATION:
APPLICANT: John, Malyakal E.
TITLE OF INVENTION: GENETICALLY ENGINEERING COTTON
TITLE OF INVENTION: PLANTS FOR ALTERED FIBER
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nicholas J. Seay, Charles & Brady
STREET: P.O. Box 2113, First Wisconsin Plaza
CITY: Madison
STATE: Wisconsin
COUNTRY: USA
ZIP: 53701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/298,687A
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/617,239
FILING DATE: 21-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/253,243
FILING DATE: 04-OC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,386
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 243-2478
TELEFAX: (608) 251-5139
INFORMATION FOR SEQ. ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 989 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Gossypium hirsutum
STRAIN: Coker 312
DEVELOPMENTAL STAGE: 10 day old fiber cells
TISSUE TYPE: fiber cells
IMMEDIATE SOURCE:
LIBRARY: CKEB10
CLONE: A11
US-08-298-687A-7

Alignment Scores:
Pred. No.: 2.42e-13 Length: 989

Score: 194.00 Matches: 55
Percent Similarity: 44.55% Conservation: 35
Best Local Similarity: 27.24% Mismatches: 58
Query Match: 12.42% Indels: 54
DB: caps: 10

US-09-624-670-63 (1 292) x US-08-298-687A-7 (1 989)

115 ValLeuTPrP-----TyrTyrPheSerLysLeuValGluPheLeuAspThrIle 141
DB 907 GTCTTTCTTGGGATATATATTTTCTTCTGCAAGATTCTTATTTATGACACCTTT 848
OY 132 PhePheValLeuAlaGlySerThrAsnGlnIleThrPheLeuHisValTyrHisAla 151
DB 847 TTATATCTCTCAAGATGATATGATATGATATGATATGATATGATATGATATGAT 788
OY 152 SerMetPheAsnIleGlyPheCysValLeuAsnTrpIleProCysGlyGlnSerPhePhe 171
DB 787 ATGCTGTCATCAT 747
OY 172 GlyProThrLeu-----AsnSerPheIleHisIleLeuMetTyrSerTyrGlyLeu 189
DB 746 CCGATGCTGCTGATATGATATGATATGATATGATATGATATGATATGATATGAT 677
OY 190 SerValIleProSerMetHisLysTyrLeuTyrPheLysSerTyrLeuThrIleAsn 209
DB 676 TGATGCTTG---GATATATGATATGATATGATATGATATGATATGATATGAT 626
OY 210 LeuValGlnPhe-----ValLeuThrIleThrHisThrLeu 221
DB 625 CTGCTGACATGCTGCTGATATGATATGATATGATATGATATGATATGATATGAT 566
OY 222 SerAlaValValGlyProTyrGlyPheProPheGlyCys-----LeuIle 236
DB 565 GCTTCT-----GGCTGCTGCTGATATGATATGATATGATATGATATGAT 533
OY 237 PheClnSerSerTyrMetMetThrLeuValIleLeuPheLeuAsnThrLeuIle 256
DB 532 TTATATGATATGATATGATATGATATGATATGATATGATATGATATGATATGAT 473
OY 257 TyrAlaGlySerProValGlySerGlnLeuGlnIleValIleValAsn----- 273
DB 472 TAC-----TGCATCAATGCAAGATGCTTCAAGCTGATCAATATCA 434
OY 274-----GlyPheProLysAlaHisIleLeuVal 282
DB 433 TTATATATGATATGATATGATATGATATGATATGATATGATATGATATGATAT 374
OY 283 AlaAsn 284
DB 473 GTTCA 468

RESULT 10

US-08-540-797-6 (2)

Sequence 6, Application US/09540797

Patent No. 5597718

GENERAL INFORMATION:

APPLICANT: Imbeck, Paul F.

APPLICANT: Imbeck, Paul F.

TITLE OF INVENTION: GENETICALLY ENGINEERED COTTON PLANTS

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: Qualites and Brady

STREET: P.O. BOX 2113

CITY: MADISON

STATE: WISCONSIN

COUNTRY: U.S.A.

ZIP: 53701

COMPUTER READABLE FORM: 4.50 inch, 800kb storage

COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09540797
FILING DATE: 20-SEP-1995
CLASSIFICATION: B00
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/617,249
FILING DATE: 21-NOV-90
APPLICATION NUMBER: US 07/254,243
FILING DATE: 04-OCT-88
ATTORNEY/AGENT INFORMATION:
NAME: Nicholas J. Seay
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 112290245
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 989 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA TO mRNA
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGIN: SOURCE:
ORGANISM: Gossypium hirsutum
STRAIN: Coker 312
DEVELOPMENTAL STAGE: 10 day old fiber cells
TISSUE TYPE: fiber cells
IMMEDIATE SOURCE:
LIBRARY: KPH10
CLONE: All

US-08-540-797-6

Alignment Scores:

pred. No.: 2,426-13 Length: 989
Score: 194.00 Matches: 55
Percent Similarity: 44.55% Conservation: 35
Best Local Similarity: 27.24% Mismatches: 58
Query Match: 12.42% Indels: 54
DB: caps: 10

US-09-624-670-63 (1 292) x US-08-540-797-6 (1 989)

115 ValLeuTPrP-----TyrTyrPheSerLysLeuValGluPheLeuAspThrIle 141
DB 907 GTCTTTCTTGGGATATATATTTTCTTCTGCAAGATTCTTATTTATGACACCTTT 848
OY 132 PhePheValLeuAlaGlySerThrAsnGlnIleThrPheLeuHisValTyrHisAla 151
DB 847 TTATATCTCTCAAGATGATATGATATGATATGATATGATATGATATGATATGAT 788
OY 152 SerMetPheAsnIleGlyPheCysValLeuAsnTrpIleProCysGlyGlnSerPhePhe 171
DB 787 ATGCTGTCATCAT 747
OY 172 GlyProThrLeu-----AsnSerPheIleHisIleLeuMetTyrSerTyrGlyLeu 189
DB 746 CCGATGCTGCTGATATGATATGATATGATATGATATGATATGATATGATATGAT 677
OY 190 SerValIleProSerMetHisLysTyrLeuTyrPheLysSerTyrLeuThrIleAsn 209
DB 676 TGATGCTTG---GATATATGATATGATATGATATGATATGATATGATATGAT 626
OY 210 LeuValGlnPhe-----ValLeuThrIleThrHisThrLeu 221
DB 625 CTGCTGACATGCTGCTGATATGATATGATATGATATGATATGATATGATATGAT 566
OY 222 SerAlaValValGlyProTyrGlyPheProPheGlyCys-----LeuIle 236
DB 565 GCTTCT-----GGCTGCTGCTGATATGATATGATATGATATGATATGAT 533

Mon Jun 16 09:01:12 2003

us-09-624-670-63.rn

Page 13

[illegible]

EARLIER FILING DATE: 1997 06 13
 EARLIER APPLICATION NUMBER: 60/061,060
 EARLIER FILING DATE: 1997 10 02

Alignment Scores:

Prod. No.: 2,790 06 Length: 834
 Score: 132.00 Matches: 32
 Percent Similarity: 51.92% Conservative: 22
 Best Local Similarity: 40.17% Mismatches: 46
 Query Match: 8.42% Indels: 4
 DB: 4 Gaps: 3

US-09-624-670-63 (1 292) x US-09-149-476-259 (1-814)

QY 2 GluGluLeuLysAlaIlePheAspAsnGluValAsnAlaPheLeuAspAsnMetPheGlyPro 21
 DB 14 GAGTCTTACGCGAGATGAGAGCTGTGTGCACTTATATCAAGATGATG---AGGAC 90
 QY 22 ArgAspSerAlaValAlaGlyTyrPheLeuLeuAspSer TyrLeuProThrPhe 39
 DB 91 GCAATATCCGAGATGAGAGCTGCTGATGAGTGGTCCGCTGCTGTAATGACCTGATT 150
 QY 40 IleLeuThrIleThrTyrLeuLeuSerIleTyrPheGlyValAsnLysTyrMetLysAsnArg 59
 DB 151 CTCTGACCTACGAGTACCTGCTT---CTCTACCTGGGCTGCTATCAATGCTAAATGCT 207
 QY 60 ProAlaLeuSerLeuAlaGlyIleLeuThrLeuTyrAsnLeuAlaIleThrLeuLeuSer 79
 DB 208 AAGGCTTCGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 267
 QY 80 AlaTyrMetLeuValIleLeuIleLeuSerSerTyrPheGlyTyrAsnLeuGlnLys 99
 DB 248 CTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 327
 QY 100 GluAsnLeuAsp 163
 DB 328 GACCTCAACAGC 339

RESULT 14

US-09-172-108-45
 Sequence 45, Application US/09122108
 Patent No. 6160104
 GENERAL INFORMATION:
 APPLICANT: Cunningham, Mary Jane
 APPLICANT: Panzer, Scott R.
 APPLICANT: Sellhammer, Jeffrey J.
 TITLE OF INVENTION: MARKERS FOR PROXIMAL PROLIFERATORS
 FILE REFERENCE: PA-0012 US
 CURRENT APPLICATION NUMBER: US/09/172-108
 CURRENT FILING DATE: 1998 10 14
 NUMBER OF SEQ ID NOS: 56
 SOFTWARE: PERL Program
 SEQ ID NO 45
 LENGTH: 124
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: unsure
 LOCATION: 34, 53, 87, 109, 122
 OTHER INFORMATION: a or g or c or t, unknown, or other
 FEATURE:
 OTHER INFORMATION: 70054590541
 US-09-172-108-45

Alignment Scores:

Prod. No.: 3,16 06 Length: 124
 Score: 121.00 Matches: 25
 Percent Similarity: 66.67% Conservative: 1
 Best Local Similarity: 64.10% Mismatches: 12
 Query Match: 7.72% Indels: 1
 DB: 4 Gaps: 3

US-09-624-670-63 (1 292) x US-09-172-108-45 (1 124)

QY 198 TyrLeuIlePheGlySerTyrLeuThrGlnAlaThrLeuValAsnThrPheVal MetThr 217
 DB 3 TACCTGCGGAGGAGAGAGATGATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 62
 QY 217 cThrIleThrLeuSerAlaValValLysSerGlySerPheProIleGlyTyrLeu 249
 DB 63 CATCAACAGCAGCTGCGAGGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 117

RESULT 15

US-08-417-330A-15
 Sequence 15, Application US/08417330A
 Patent No. 5719057
 GENERAL INFORMATION:
 APPLICANT: BADENHORN, KAREN
 APPLICANT: LE FROEDELLES, BEATRICE
 APPLICANT: WHITTING, PAUL
 APPLICANT: WINGROVE, PETER
 TITLE OF INVENTION: STABLY TRANSCRIPTED CELL LINE EXPRESSING
 TITLE OF INVENTION: GABA-A RECEPTOR AND NOVEL CLONED
 TITLE OF INVENTION: GABA-A RECEPTOR SUBUNIT cDNA SEQUENCES
 NUMBER OF SEQUENCES: 20
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: J. MARK HAND - MEROX & CO., INC.,
 STREET: 126 EAST LINCOLN AVENUE P.O. BOX 2000
 CITY: RAINWAY
 STATE: NJ
 COUNTRY: US
 ZIP: 07065-0900
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/417, 330A
 FILING DATE: 05-Apr-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: HAND, MARK
 REGISTRATION NUMBER: 36,545
 REFERENCE/WORK NUMBER: 711091A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 908-594-3905
 TELEFAX: 908-594-4720
 TELEX:
 INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2310 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: Coding Sequence
 LOCATION: 298...1683
 OTHER INFORMATION:
 US-08-417-330A-15

Alignment Scores:

Prod. No.: 0,073 Length: 2410
 Score: 100.00 Matches: 59
 Percent Similarity: 35.00% Conservative: 54
 Best Local Similarity: 18.44% Mismatches: 108
 Query Match: 6.38% Indels: 101
 DB: 1 Gaps: 11

US-09-624-670-63 (1-292) x US-08-417-330A-15 (1 2410)

Mon Jun 16 09:01:12 2003

us-09-624-670-63.rn1

Page 15

QY 28 GlyTyrPheLeuLeuAspSerTyrLeuProThrPheIleuThrIlePheTyrLeuLeu 47
D 1069 GgCTACTTGTGCTACACACCTTACCTCCGCTATATACGCTGTATCTTATCAGAGGTG 1128
QY 48 SerIleThrLeuGlyAsnLysTyrMetLysAsnArgProAlaLeuSerLeuArgIle 67
D 1129 TCCTTTGGCTGACACCGCAATCAGCCAGACACTTTTGGCGTACACCGCTG 1188
QY 68 LeuThrLeuTyrAsnLeuAlaIleThrLeuLeuSerAlaTyrMetLeuValGluLeu 87
D 1189 CTGACCATGACGCTCAGCATCAGCCGAGAACTCTGCCCCAAAGTGGCTAGGCC 1248
QY 88 LeuSer--SerThrPglucIyGlyTyrAsnLeuGlnCysGlyAsnLeuAspSerAlaGly 106
D 1249 ACCGCCATGAGCTGG----- 1263
QY 107 GluGlyAspValArgValAlaLysValLeuThrPrtPrtTyrTyrPheSerLysLeuValGlu 126
D 1264 -----TTTCATAGCTGTGTCTATGCTTGTCTGCGCTGTATAG 1308
QY 127 PheLeuAspThrIlePhePhe----- 133
D 1309 TTGGCAGGCTCATTTACTTTACCAAGAGAGCTGGCCGTGAGTGCAGAAAAAGCCTG 1368
QY 134 -----ValLeuArgLysLysThrAsnGlnIle 142
D 1369 GAAAGCAGCCAGATCAGAAAAAGCGTGAAGTCACTACTATTAATGATCAAAACGCTTT 1428
QY 143 ThrPheLeuHisValTyrHisHisAlaSerMetPheAsnIleThrPrtPrtCysValLeuAsn 162
D 1429 ACAACTGGGAGAGTGTCTCACCCCAAC----- 1458
QY 163 TrpIleProCysGlyGlnSerPhePheGlyProThrLeuAsnSerPheIleHisIle--- 181
D 1459 --ATTCCGAGAACAGACCCGAGGAGCGTCAATACAACTCAGCTCAGTAA 1515
QY 182 -----LeuMetTyrSerTyrTyrGlyLeuSer----- 190
D 1516 CCCTTGAAAGACAACTCTGAAAGCAAAAAAGCACTTACAACTTACAGCAAAATGAC 1575
QY 191 -----ValPheProSerMet-----HisLysTyrLeuThrPrtPrtLys 202
D 1576 AAAATGTCCGAAATGCTATTCACACTTGTTCGCACTTTCACAACTTACGTTTACTGGCA 1635
QY 203 LysTyrLeuThrGlnAlaGlnLeuValGlnPhe----- 213
D 1636 ACGTATTGATGATGAGCGCGGTGATAAAGG-AGCGCGCTCTCCAAAATMACGGCCAC 1694
QY 214 -----ValLeuThrIleThrHisThrLeuSerAlaValLysProCysGlyPhe--- 230
D 1695 ACTCCGAAACTCCAGACAGCAGCATAGCTTCAGCGAAATGTACCCAGAGAGAGGTTTGCT 1754
QY 231 -----PropheGlyCysLeuIlePheGlnSerTyrMetLeuThrLeuVal 246
D 1755 CACAGGAGCTCCATATGTGACCACTTTCAGGAAATTTTTCATGTTTATATATA 1814
QY 247 -----IleLeuPheLeuAsnPheTyr-IleGlnThrTyrPrtPrtLys 260
D 1815 TGTACAAATATATGCTTGATGATTTCTA--TATGTAACCTTCAGATGTTCCAAAGATG 1871
QY 260 sproValLysLysGlnLeuGlnLysGlnLysValLysAsnGlyPheProLysAlaHis 279
D 1872 TCCCATGTATATTCGACAAACAACTTCTGAAAAACAGATGATGACTGACAC 1929

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Job time : 61.3604 secs

1
2
3

GenCore version 5.1.6
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OW protein - nucleic search, using frame_plus.p2n model

Run on: June 15, 2003, 23 02 06 Search time 127 966 seconds
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3304.262 Million cell updates/sec

Title: US-09-624-670-63

Partial score: 1567
Sequence: 1 MEQLAFDEYNAFLDNNEG.....NGEPKHH IVANNMTTKRAQ 292

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1029858 seqs, 724030393 residues

Total number of hits satisfying the search parameters: 2459716

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters: -DB=xlp
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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAEXT=0.5 -DELOP=6 -DELEXT=7

Database: Published Applications NA:

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2. /cgn2.6/ptodata/1/pubpna/PC1_NEW_PUB.seq.*
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4. /cgn2.6/ptodata/1/pubpna/US06_PUBCMB.seq.*
5. /cgn2.6/ptodata/1/pubpna/US07_NEW_PUBCMB.seq.*
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10. /cgn2.6/ptodata/1/pubpna/US09_PUBCMB.seq.*
11. /cgn2.6/ptodata/1/pubpna/US10_NEW_PUBCMB.seq.*
12. /cgn2.6/ptodata/1/pubpna/US10_PUBCMB.seq.*
13. /cgn2.6/ptodata/1/pubpna/US06_NEW_PUBCMB.seq.*
14. /cgn2.6/ptodata/1/pubpna/US06_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1567	100.0	879	9	US-09-849-199A-22
2	1567	100.0	879	10	US-09-903-456-5
3	1431	91.3	2426	9	US-10-198-846-13406
4	956	5	61	0	US-09-903-456-6

5	941.5	60.1	914	10	US-09-903-456-4	Sequence 3, Appl
6	749	47.8	748	9	US-09-764-868-352	Sequence 352, App
7	670.5	42.8	871	9	US-09-764-868-353	Sequence 353, App
8	462.5	29.5	1492	9	US-09-809-391-258	Sequence 258, App
9	462.5	29.5	1542	9	US-09-809-391-106	Sequence 106, App
10	420.5	26.8	1680	10	US-04-822-830A-145	Sequence 145, App
11	403.5	25.7	819	10	US-09-903-456-7	Sequence 7, Appl
12	403.5	25.7	819	10	US-09-903-456-72	Sequence 72, Appl
13	401.5	25.6	819	10	US-09-903-456-70	Sequence 70, Appl
14	399.5	25.5	819	10	US-09-903-456-73	Sequence 73, Appl
15	397.5	25.4	2225	10	US-09-925-301-248	Sequence 248, Appl
16	397	25.3	957	10	US-09-903-456-2	Sequence 2, Appl
17	396.5	25.3	818	10	US-09-903-456-71	Sequence 71, Appl
18	394.5	25.2	819	10	US-09-903-456-69	Sequence 69, Appl
19	393.5	25.1	819	10	US-09-903-456-74	Sequence 74, Appl
20	375	23.3	549	9	US-09-931-316-1727	Sequence 1727, App
21	368	23.5	24664	9	US-10-073-951-613	Sequence 613, App
22	368	23.5	24664	10	US-09-764-867-613	Sequence 17480, A
23	348	22.2	430	9	US-09-918-995-17480	Sequence 37438, A
24	329	21.0	384	9	US-09-918-995-37438	Sequence 67, Appl
25	306	19.5	630	10	US-09-903-456-67	Sequence 9957, Ap
26	305.5	19.5	447	9	US-09-918-946-9457	Sequence 1, Appl
27	279	17.8	954	10	US-09-903-456-1	Sequence 1, Appl
28	267	17.0	194	10	US-09-864-761-194	Sequence 194, A
29	267	17.0	194	10	US-09-864-761-194	Sequence 26863, A
30	267	17.0	409	10	US-09-864-761-194	Sequence 13059, A
31	267	17.0	485	10	US-09-864-761-194	Sequence 2289, Ap
32	267	17.0	8861	9	US-09-764-868-1445	Sequence 1445, Ap
33	265	16.9	455	10	US-09-864-761-194	Sequence 10375, A
34	235	15.0	587	10	US-09-903-456-16	Sequence 16, Appl
35	232	14.8	590	10	US-09-903-456-17	Sequence 17, Appl
36	209	13.3	867	10	US-09-903-456-4	Sequence 4, Appl
37	209.5	12.8	795	9	US-09-759-1308-222	Sequence 222, Appl
38	209.5	12.8	798	10	US-09-903-456-63	Sequence 63, Appl
39	209.5	12.8	2775	9	US-10-161-521A-3	Sequence 3, Appl
40	200.5	12.8	2989	9	US-09-759-1308-221	Sequence 221, App
41	196	12.5	813	9	US-09-759-1308-238	Sequence 238, App
42	161	10.3	2932	9	US-09-759-1308-241	Sequence 241, App
43	160.5	10.2	922	9	US-09-759-1308-242	Sequence 242, App
44	158.5	10.1	511	9	US-09-918-946-10797	Sequence 10797, A
45	155	9.9	167	10	US-09-783-590-46	Sequence 46, Appl

ALIGNMENTS

RESULT 1
US-09-849-199A-22
Sequence 22, Application US/09849199A
Publication No. US29030082754A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pradip
APPLICANT: Thurmond, Jennifer M.
APPLICANT: Huang, Yung-Sheng
APPLICANT: Das, Tapas
TITLE OF INVENTION: DELTA 4-THESATPRASE GENES AND USES
TITLE OF INVENTION: THEPROOF
FILE REFERENCE: 6804 US-01
CURRENT APPLICATION NUMBER: US/09/849,199A
CURRENT FILING DATE: 2002-04-15
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 22
LENGTH: 879
TYPE: DNA
ORGANISM: Mus musculus
US-09-849-199A-22
Alignment Scores:
Pred No: 789, 169
Score: 1567.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Matches: 879
Mismatch: 292
Mismatches: 0

Query Match:	100.00%	Indels:	
DB:	g	Gaps:	
US-09-624 670 64 (1.29%) x US-09 849 199A.22 (1.87%)			

QY		22	LeuseALaValAllyllystrcygslPheProPhagIyCysLlelllePhnCISSrSe	240
Dd		661	CTAGTCCCGGTGGTCGAAGCCCTGTCGCTTCCCCTTGCGTCGTCATCTTGCATTTCG	720
QY		241	TyrMetMetThrLauValIlleuDeHeuLeuSnpheryrlleslnThryrAylLySlys	260
Dd		721	TATATGATACGGTGGTCATCTGTTCTTAACCTCATATTCAGACAATACGGAAAAAG	780
QY		261	PrvAlalyslsqLueuclngLueysgluVallylasnsglylPheProLysAlahlsleu	280
Dd		781	CCAGTGAAGAAGAGCTGCAGAGAAGAAGTGAAGAATGTTTCCCCAAAGGCCACTTA	840
QY		281	IlevalAlasnclyMelThrsplysLysAlJcGln	292
Dd		841	ATTGTGCTAATGCGATGCAAGGAGAACGAAGCGCTCAA	876
		RESULT 3		
		US-10-198-846-13406		
		/ Sequence 13406, Application US/10198846		
		/ Publication No. US20030059974A1		
		GENERAL INFORMATION:		
		APPLICANT: Lillie, James		
		APPLICANT: Xu, Yondyao		
		APPLICANT: Wang, Youzheng		
		APPLICANT: Stelmann, Kathleen		
		TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS		
		TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND		
		TITLE OF INVENTION: THERAPY OF BREAST CANCER		
		FILE REFERENCE: MRI-049		
		CURRENT APPLICATION NUMBER: US/10/198, 846		
		CURRENT FILING DATE: 2002-07-18		
		PRIOR APPLICATION NUMBERS: 60/306, 220		
		NUMBER OF SEQ. ID NOS: 14084		
		SOFTWARE: FASTSeq for Windows Version 4.0		
		SEQ ID NO 13406		
		LENGTH: 2426		
		TYPE: DNA		
		ORGANISM: Homo sapiens		
		FEATURE:		
		NAME/KEY: misc.feature		
		LOCATION: 1..2426, 2426		
		OTHER INFORMATION: n = A,T,C or G		
		(S-10-198-846-13406		
		Alignment Scores:		
		Pred. No.: 1,18e-152		2426
		Score: 1431.00		Matches: 262
		Percent Similarity: 93.92%		Conservative: 16
		Host local Similarity: 86.51%		Mismatches: 14
		Query Match: 91.32%		Indels: 4
		DB: 9		Gaps: 1
US-09-624-670-63 (1-292) x US-10-198-846-13406 (1-2426)				
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Dd		85	ATGCAACATCTAAAGCCCTTGATGATGATAAATCAATGCTTTTTGGCAAAATATTTGGA	144
2Y		21	ProAraspserArayAlarGcllylrPpheLeuLeuAspseryrLeuProthrPheIle	40
Dd		145	CCGGCAATTCCTCGACATCGACGACAGGGGTGTTCACGTHGACTGTAACTTTCCTACTTTTTT	204
QY		41	LeuThrIleThrrTyrrLeuLeuSerIlelrTripleugLysLnlySYrMet_YsasnarPro	60
Dd		205	CTTACTTCTCATGATATTTGCTTCAATATGGCTGGGTAAACAGTATATGACAGACCT	264
QY		61	AlaleuserLeuArGcllylleuThrleuLyrasnleuAlaleThrleuLeuSeraIa	80
Dd		265	GCCTTTCCTCTCAGGGGATNCCCTCACCTTGATATCTTTGGAACTACACACTTCTCCGCC	324
QY		81	TyrMetleuValleuLleuleuLeuSerTrprgluglyglyTYrrasnleuSlncysGln	100

[illegible]


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QY 208 aglnleuValGlnPheValLeuThrIleThrIleSerAlaValValLysProCy 228
    |||||
    187 GCAGCTGCTTCACCTTGGCTGACAACTATGATACCTGCGGCGTGCATCTGCGCGG 246
    |||||
QY 228 sglyPheProPheGlyCysLeuIlePheGlnSerSerTyrMetLeuThrLeuValIleLe 248
    |||||
    247 CACATTCCCTCTTGGTGGTGTATTTCATGATGGATACATGATTCCCTGATTGCTCT 306
    |||||
QY 248 upheleuAsnPheTyrIleGlnThrTyrArgLysLysProValIlyslsGluLeuGlnI 268
    |||||
    307 CTTCACAAACTTCTACATTGAGCCTACACACAGAAAGGGGCTGCCGAGGAAAGACCA 366
    |||||
QY 268 u--LysGluValLysAsnGlyPheProLysAlaHisLeuIleValAlaAsnGlyMetTh 287
    |||||
    367 CCGAAGGAGCAACACCAATGCG-----TCCATGGCTGCTGTGATGCGACACAC 414
    |||||
QY 287 rAsp 288
    |||||
Db 415 CAAG 418
```

Search completed: June 16, 2003, 01:12:52
Job time : 134.966 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

Ok protein - nucleic search, using frame_plus_p2n model

Run on: June 15, 2003, 21:36:46 ; Search time 163.06 Seconds

(without alignments)
4066.072 Million cell updates/sec

Title: US-09-624-670-63
Perfect score: 1567
Sequence: 1 MEOLKAFDEVNAFLINMEG. NCPEKAIIVAN:MTUKKQ 292

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Zgapop 6.0, Zgapext 7.0
Delop 6.0, Delext 7.0

Searched: 16154066 seqs, 8037743376 residues

Total number of hits satisfying chosen parameters: 32108132

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

MODE=frame_plus_p2n_model -REV=1p
-O=/cgn2_1/USPTO.spool/US09624670/runat_1064003_075430_11642/app-query.fasta.1.110
-DB=EST -QPM=fastap -SUFFIX=tbl -MINMATCH=0.1 -LOOPEL=0 -LPOPEXT=0
-UNITS=bits -START=1 -END=1 -MATP=blonsum62 -TRANS=human40.cgi -LIST=45
-DOCALLIGN=200 -THR_SCORE=tbl -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=tbl -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09624670.ecgn.1.13724.arnat_11062003_075430_11642 -NCPU=6 -ICU=3
-NO_MMAP -LARGEQUERY -NRC_SCORES=0 -WAIT -DSPLOCK=100 -LONLOCK
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -YGAPOP=6
-YGAPEXT=7 -ZGAPOP=10 -ZGAPEXT=0.5 -DELCP=6 -DELEXT=7

Database:

EST.*
1: em_vslha.*
2: em_gschum.*
3: em_eslin.*
4: em_eslin.*
5: em_eslin.*
6: em_eslin.*
7: em_eslin.*
8: em_eslin.*
9: qb_eslin.*
10: qb_eslin.*
11: qb_hic.*
12: qb_est3.*
13: qb_est4.*
14: qb_est5.*
15: em_estlin.*
16: em_estlin.*
17: qb_gss.*
18: em_gss_hum.*
19: em_gss_inv.*
20: em_gss_pln.*
21: em_gss_vit.*
22: em_gss_lun.*
23: em_gss_mam.*
24: em_gss_mus.*
25: em_gss_other.*
26: em_gss_pro.*
27: em_gss_rod.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1564	99.7	3800	11 AK014803	AK014803 Mus musculus
2	1414	99.2	1150	13 BM461375	BM461375 AGNCNCOURT
3	1097	70.6	661	10 BB544040	BB544040 BB544040
4	1079	68.9	642	10 BB516155	BB516155 BB516155
5	1015	64.8	589	9 AT172603	AT172603 MT-P-23P
6	1008	64.3	684	13 B1598800	B1598800 B01245579
7	994	63.4	673	10 BB442836	BB442836 BB442836
8	962	61.4	645	10 BB441301	BB441301 BB441301
9	929	59.3	629	13 R1302770	R1302770 PPI10 PK0
10	922.5	58.9	941	9 AL559414	AL559414 AL559414
11	904	57.7	537	12 BE949059	BE949059 U1-M-BH3
12	903.5	57.7	1088	12 BE778035	BE778035 B01461148
13	896	57.2	950	9 AL553407	AL553407 AL553407
14	887	56.6	861	9 AL514872	AL514872 AL514872
15	886	56.5	807	14 B2883263	B2883263 AGNCNCOURT
16	885	56.5	521	10 AW484100	AW484100 U1-M-BH3
17	879	56.1	631	9 AL5595258	AL5595258 M143501.Y
18	879	56.1	893	14 HQ217076	HQ217076 AGNCNCOURT
19	877	56.0	504	12 HP461032	HP461032 U1-M-CGUP
20	871.5	55.6	900	13 B1593107	B1593107 B03344472
21	844.5	53.8	700	13 B155440	B155440 B03403816
22	840	53.8	619	9 AL760814	AL760814 AL760814
23	834	53.2	464	9 AL428150	AL428150 M143501.X
24	833	53.2	991	14 PQ895704	PQ895704 AGNCNCOURT
25	822	52.5	661	10 BB581068	BB581068 B04 B1962
26	811	51.5	745	9 A0079897	A0079897 A0079897
27	807	51.5	802	9 AL516234	AL516234 AL516234
28	802	51.2	499	9 AT225632	AT225632 U13111.Y
29	800.5	51.1	825	13 B1853179	B1853179 B03379527
30	792	50.5	607	13 B1559494	B1559494 B03246113
31	787	50.2	760	9 AL548756	AL548756 AL548756
32	785	50.1	461	12 HP470691	HP470691 U1-M-BH3
33	781.5	49.4	847	14 B2113770	B2113770 AGNCNCOURT
34	781	49.4	787	13 R1597218	R1597218 B01250946
35	765	48.8	525	12 BG813561	BG813561 B0440407
36	764.5	48.8	884	13 B1785856	B1785856 B0340096
37	759	48.4	712	13 B2523961	B2523961 B0123961
38	754	48.1	445	9 A1815460	A1815460 B04604.Y
39	754	48.1	932	9 AL552819	AL552819 AL552819
40	744	47.5	862	13 B1635075	B1635075 B03087730
41	726.5	46.4	810	12 BG251449	BG251449 B03363905
42	714	45.6	748	12 BQ270622	BQ270622 B06609.Y
43	709.5	45.3	712	13 B2375432	B2375432 B03841085
44	706	45.1	961	14 B0346171	B0346171 AGNCNCOURT
45	706	45.0	927	12 B0133950	B0133950 B03344023

ALIGNMENTS

RESULT 1
AK014803
LOCUS
DEFINITION
AK014803 3800 bp mRNA linear HTG 19-FAN-2002
Mus musculus adult male testis cDNA, RIKEN full-length enriched
library, clone:4921503C7, subcloning of very long chain fatty acids
(FEN1/B102, SUB4/E103, yeast) like 2, full insert sequence.

ACCESSION
AK014803
VERSION
AK014803.1 GI:12852861
KEYWORDS
HTG; CAP trapper;
SOURCE
Mus musculus (strain:G57BL/6J) adult male testis cDNA to mRNA,
clone:4921503C17.

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE	Carninci, P. and Hayashizaki, Y.
TITLE	High efficiency full length cDNA cloning
JOURNAL	Methods, Enzymol., 403, 19-44 (1999)
DOI	10.1016/S0076-6809(99)90254-3
REFERENCE	
AUTHORS	2
TITLE	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Komori, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
JOURNAL	Genome Res., 10 (10), 1617-1630 (2000)
DOI	10.1093/genres.10.10.1617
REFERENCE	
AUTHORS	3
TITLE	Shibata, K., Itoh, M., Aizawa, K., Naraoka, S., Sasaki, N., Carninci, P., Komori, H., Akiyama, J., Nishi, K., Kitsumata, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishio, T., Harada, A., Yamamoto, R., Matsumoto, H., Sadaquchi, S., Ikegami, T., Kashiwagi, K., Yonida, Y., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M., Honda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuda, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and Hayashizaki, Y.
JOURNAL	RIKEN integrated sequence analysis (RISA) system 384-format sequencing pipeline with 484 multiplexillary sequencer
DOI	Genome Res., 10 (11), 1757-1771 (2000)
REFERENCE	
AUTHORS	4
TITLE	Kawai, J., Shibata, K., Hayashizaki, Y., Komori, M., Itoh, M., Ishii, Y., Aizawa, K., Iizawa, M., Nishi, K., Kiyosawa, H., Komori, S., Yamada, A., Saito, T., Okazaki, Y., Gajboreti, T., Honjo, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batilov, S., Casavant, T., Fleischmann, W., Gastroland, T., Gissi, C., King, B., Kochiwa, H., Kuchi, P., Lewis, S., Matsuo, Y., Nika, D., Plesio, G., Quackenbush, J., Schmitt, L. M., Staehli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okada, T., Furuno, M., Aono, H., Baldarelli, R., Barish, G., Blake, J., Bottelli, D., Boljund, N., Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bolte, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, J. A., Kamiya, M., Lee, N. P., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, L., Mombassi, P., Nordone, P., Rijn, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schombach, J., Segal, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyooka, K., Wang, K. H., Wolitz, C., Whittaker, C., Wilming, L., Wyshynski, B. J., Yoshida, K., Hasegawa, Y., Kawai, J., Kohsaki, S. and Hayashizaki, Y.
JOURNAL	Functional annotation of a full length mouse cDNA collection
DOI	Nature, 409 (6821), 685-690 (2001)
REFERENCE	
AUTHORS	5 (bases 1 to 4800)
TITLE	Arakawa, T., Baldarelli, R., Itoh, M., Brownstein, M., Bull, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Hume, D., Imoto, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Komori, H., Kouda, M., Koya, S., Kuribata, C., Matsuyama, I., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Saito, H., Saito, P., Sakai, K., Sakai, K., Sano, H., Sasaki, D., Schmitt, L., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sugabe, Y., Suzuki, H., Tagami, M., Tadawa, A., Takahashi, F., Tanaka, T., Tojima, Y., Toya, T., Yamamura, T., Yamada, J., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
JOURNAL	Direct submission
DOI	Submitted (10-Jul 2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), 1-7-22 Suicho-cho, Wako-shi, Saitama-ken, Yokohama, Kanagawa 240 0045, Japan (E-mail: genome-res@sc.riken.go.jp, URL: http://genome-res.riken.go.jp/ Tel: 81 47 601 4222)

COMMENT: Fax:81-45-503 9216)
Further details:
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer
15' GAGCAGACGAGCATCCACAGACCTCTTTTCTTTTTCV 3', cDNA was prepared by using trehalose thermo activated reverse transcriptase and subsequently enriched for full-length by cap trapper. Second strand cDNA was prepared with the primer adapter of sequence 15' CAGAGAACAATTCAGATTAAATAAATAATTAATGGGGCCCCCG 3'. cDNA was cleaved with BamH1 and XhoI. cDNA of size comprised longer than 7 kb was selected before cloning. Vector: a modified phagescript KS(+)-after bulk excision from lambda phage. Cloning sites: 5' end: SalI; 3' end: BamH1. Host: DH10b.
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/db_xref="MIM:MIM:1907096"
/db_xref="taxon:100960"
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/sex="male"
/tissue_type="testis"
/clone_lib="RIKEN full length enriched mouse cDNA library"
/cov_stage="adult"
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177..1004
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/gene="Elovl2"
/note="putative"
3800
/gene="Elovl2"
/note="putative"
BASE COUNT 1001 a 885 c 819 g 1095 t
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Scores: 1562.00 Match: 291
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatch: 0
Query Match: 99.68% Indels: 0
DH: 11 Gaps: 0
ms-09-624-670-63 (1292) x AWC14093 (13929)

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 D 249 ACCATCAAGTACGCTGCTCGATATGCGGTACCAAGTACATGACATAGAGAGAGGCTGCT 308
 QY 62 LeuSerLeuArgGlyIleLeuThrIleTyrAsnLeuAlaIleIleLeuLeuSerAlaTyr 81
 D 309 CTGTCTCTCAGGGGAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 468
 QY 82 MetLeuValGluLeuIleLeuSerSerTyrGluGlyIleTyrAsnLeuGlnIleGlnAsn 101
 D 369 ATGCTGGTGGAGCTGATCT 426
 QY 102 LeuAspSerAlaClyIleGluGlyAspValArgValAlaIleValLeuIleTyrIleTyrPhe 121
 D 429 CTGACAGAGTGCAG 488
 QY 122 SerIleLeuValGluPheLeuAspThrIlePhePheValIleArgIleIleSerIleGln 141
 D 489 TCCAACTAGTACGATCT 548
 QY 142 IleThrPheLeuHisValIleThrHisIleAlaSerMetPheAsnIleIleTyrIlePhe 161
 D 549 ATCACT 608
 QY 162 AsnTyrIleProCysGlyIleSerPhePheGlyProThrLeuAsnSerPheIleIleIle 181
 D 609 AACTGATACCT 668
 QY 182 LeuMetIleSerTyrIleGlyLeuSerValPheProSerMetHisIleIleIleIleIle 201
 D 669 CTGATGATACCT 728
 QY 202 IlyIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 221
 D 729 AACAGAGTACCTGACAG 786
 QY 222 SerAlaValIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 241
 D 789 AGTCCCTGCTGAG 848
 QY 242 MetMetThrIleValIleLeuPheLeuAsnPheIleIleIleIleIleIleIleIleIle 261
 D 849 ATGATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 908
 QY 262 ValIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 281
 D 909 GTGAG 968
 QY 282 ValIleAsnGlyMetThrAspIleIleIleIleIleIleIleIleIleIleIleIle 292
 D 969 GTGCTATATGCTATATGCTATATGCTATATGCTATATGCTATATGCTATATGCTAT 1001
 RESULT 2 1150 bp mRNA linear EST 05-FEB-2002
 3M461375
 LOCUS ACENOCURT_6419890 NCLCGAP_Ov44 Mus musculus cDNA clone
 DEFINITION IMAGE:5504127 5', mRNA sequence
 ACCESSION BM461375
 VERSION BM461375.1 GI:18510415
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 1150)
 NIH-MGC http://mgi.ncl.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: rgs@ncl.nih.gov
 Tissue Procurement: Aaron Hansen
 cDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution, MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILMN, etc.
 http://image.liml.gov
 Plate: LM412144 row: p column: 16
 High quality sequence start: 11
 High quality sequence stop: 664.
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 1. 1150
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 /clone="IMAGE:5504127"
 /lab_host="PH108 (T1 phage-resistant)"
 /note="Organ: ovary, IMS-treated; Vector:
 pCMV-SPORT6.cdb; Site: 1; PCRV; Site 2: Not; Cloned
 unidirectionally. Primer: oligo dT. Average insert size
 2.2 kb. Library constructed by Life Technologies. Note:
 this is a NCLCGAP Library."
 BASE COUNT 288 a 327 c 244 g 291 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 4,05e-152 Length: 1150
 Score: 1414.00 Matches: 274
 Percent Similarity: 97.20% Conservative: 4
 Best Local Similarity: 95.80% Mismatches: 3
 Query Match: 90.24% Indels: 5
 DB: 13 Gaps: 0
 US-09-624-670-63 (1-292) x BM461375 (1-1150)
 QY 12 AsnAlaPheLeuAspSerMetPheGlyProAlaGaspSerArgValArgGlyTyrPheLeu 31
 D 43 AATGCTTTCTTGGAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 82
 QY 32 LeuAspSerTyrIleProThrPheIleLeuThrIleThrIleLeuSerIleIleIle 51
 D 83 CTGAGAGTCAATCTTCCATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 142
 QY 52 GlyAsnIleSerMetIleAsnArgProAlaLeuSerLeuArgGlyIleLeuThrIleIle 71
 D 143 GGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 202
 QY 72 AsnLeuAlaIleIleIleLeuSerAlaTyrMetLeuValGluIleIleLeuSerSerTyr 91
 D 203 AATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 262
 QY 92 GluGlyGlyIleIleLeuGlnIleGlnIleGlnIleGlnIleGlnIleGlnIleGlnIle 111
 D 263 CAACGACGCTTCAACGCTTCAACGCTTCAACGCTTCAACGCTTCAACGCTTCAACGCT 322
 QY 112 ValAlaIleValLeuIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 131
 D 323 GTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 382
 QY 132 PhePheValLeuArgGlyIleIleIleIleIleIleIleIleIleIleIleIleIleIle 151
 D 383 TTTCTTGTCTTGGAAAAAGACATGATGATGATGATGATGATGATGATGATGATGAT 442
 QY 152 SerMetPheAsnIleIleTyrIlePheValIleAsnIleIleIleIleIleIleIleIle 171
 D 443 TCCATGCTCAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 502
 QY 172 GlyProThrLeuAsnSerPheIleIleIleIleIleIleIleIleIleIleIleIleIle 191
 D 503 GGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 562
 QY 192 PheProSerMetHisIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 211
 D 563 TTCCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 622

Tissue Procurement: Miklos Palokovits, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHRI), Shiroki
 Toshiyuki and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILN)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILN at:
<http://image.jnl.gov>
 plate: L1AM1727 row: n. column: 19
 High quality sequence stop: 669

FEATURES

SOURCE

Location/Qualifiers

1. 604

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAG:5287890"

/clone_lib="NIH_MGC_96"

/tissue_type="hypothalamus"

/lab_host="DH10B"

/note="Organ: Brain; Vector: pBluescriptR (modified
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); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3',
 size-selected for average insert size 2.3 kb and
 normalized to 10⁷ 5'. This is a primary library enriched
 for full-length clones and constructed using the
 Cap-trapper method (Carninci, in preparation). Library
 constructed by M. Brownstein (NHRI, National
 Institutes of Health). Note: this is a NIH_MGC Library."

FASTA COUNT 160 a 163 c 156 g 205 t
 CRIGIN

Alignment Scores:

Fixed No.: 1.22e-105 Length: 684
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 Percent Similarity: 95.98% Conservative: 9
 Best Local Similarity: 91.46% Mismatches: 8
 Query Match: 64.33% Indels: 0
 Gaps: 0

US-09-624-670-63 (1-292) x B1598800 (1-684)

1 MetGluInLeuLysAlaIhCASPASNCIuValAsrAlaPheLeuASPASnKcthcly 20
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 196 CTACAGTCATATCT 255
 61 AlaLeuSerLeuArgGlyIleLeuThrIleTyrAsnLeuAlaIleThrLeuLeuSerAla 80
 256 GCTTTCTCTTAAAGGATATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 315
 81 TyrMetLeuValGluLeuIleLeuSerTrpGlyGlyTyrAsnLeuIleGlyTrp 100
 316 TACGCTGCGACAGCTTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 375
 101 AsnLeuAspSerAlaGlyGlyGlyValArgValAlaIleValLeuTrpTrpTyr 120
 376 GATCTTACACCGCCAGCGCAAGCTGACATCCGGCTGACCAAGCTGCTGCTGCT 435
 121 PheSerTyrLeuValGluPheLeuAspThrIlePhePheValLeuArgTyrSylsThrAsn 140
 436 TTCTCCAAATCAGTAGATTCCTGACACCAATTTTCTCTCTTGGGAAAAAAGAGAT 495
 141 GluIleThrPheLeuHisValTyrHisAlaSerMetPheAsnIleTrpTrpCysVal 160
 496 CAGATTACTTCT 555
 161 LeuAsnTrpIleProCysGlyInsSerPhePheGlyProThrLeuAsnSerPheIleHis 180

181 IleLeuMetTyrSerTyrTyrClyLeuSerValPheProSerMetHisTyrLeu 199
 616 ATTCTATATCT 672

RESULT 7

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

JOURNAL

COMMENT

JOURNAL

COMMENT

JOURNAL

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FEATURES

SOURCE

LOCATION/Qualifiers

1. 673

/organism="Mus musculus"

/db_xref="taxon:10090"

/clone="A93004JF19"

/clone_lib="RIKEN full-length enriched, adult retina"

/tissue_type="retina"

/dev stage="adult"

/lab_host="DH10B"

/note="Site_1: SalI; Site_2: BamHI; cDNA library was

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 Best local Similarity: 76.67%
 Query Match: 57.66%
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 Conserved: 15
 Mismatches: 34
 Indels: 7
 Gaps: 2

US 09 624 670 63 (1 292) x AF78035 (1 1088)

1 MotCluInclouysalaphaAspasciValAsn AlaPhelouAspasciMetPhel 20
 DB ATGCAATCTGAAAGGCTTTGATGATGAAATCATATGCTTTTGGACAAATATGTTGG 141
 20 yprArAspserArValAractlytrpPhelouAspserTyrleuProthPhel 49
 DB ACCGCGACATCTGCACACACAGCTTCATATGACCTTACCTTACCTTACCTTACCTT 201
 40 elouThrlleThylleuPseuLleTPrleuGlyAsnLysTyrMetLysAsnPrP 60
 DB TCTTACTGTCACATATCTGCTTCATATGCTTCAGTAACTATATGACACACACAC 261
 60 GAlaLeuSerLeuAractlyleuouPhleuTyrAsnLysAlaIlePhleuouSerAl 80
 DB TCTTCTTCTTCTTCAAGATATCTTCACTTGTATATATGTAATCAACATCTCTCCG 321
 80 dlyrMetLeuValleleuouIleleuSerSerTTPGleuIlelylTyr-AsnLeuIncys 109
 DB GTACATGCTGCAACACATATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 381
 122 GTACATGCTGCAACACATATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 381
 100 InAsnLeuAspserAlMetLysleuGlyAspValAractlyleuValleleuTPrTyr 120
 DB AACATCTGAC 441
 120 yprPhSerTyrleuValleleuPhelouAspThrIlePhelouValleuAlGlyLys 140
 DB ATTTCTTCTTCAAGATATCTTCACTTGTATATATGTAATCAACATCTCTCTCTCT 501
 140 snGlnIlePhleuHisValTyrHisHisAlaSerMetPhoAsnIleTPrTPrCysV 160
 DB GTACATGCTGCAACACATATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 561
 502 GTACATGCTGCAACACATATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 561
 160 AlaLeuAspThrIlePrMetLysleuGlyAspValAractlyleuValleleuTPrTyr 180
 DB TCTTCAATCTGAAAGGCTTTGATGATGAAATCATATGCTTTTGGACAAATATGTTGG 621
 562 TCTTCAATCTGAAAGGCTTTGATGATGAAATCATATGCTTTTGGACAAATATGTTGG 621
 180 IleleuMetTyrSerTyrTyrGly-LeuSer ValPhoProSerMetHisLysTyrLe 199
 DB ACATCTTATATATCTTACTATATGACCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 681
 622 ACATCTTATATATCTTACTATATGACCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 681
 199 dlyrTPrP LysLysTyrleuThrGlnAlaGlnLeuValGlnPh-VallleuThr 217
 DB CTTCGCGCGCAATCAATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 741
 682 CTTCGCGCGCAATCAATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 741
 217 dThrHisThrleuSerAlaValIleLysProGlyGlyPh-ProPhocIleGys 234
 DB AAGCGCAACATCAAGCGCG TCCCAACCGCAACGCTTCTCTCTCTCTCTCTCTCTCT 790
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RESULT 13
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 Locus
 DEFINITION AL553407 t11 NEL006 p12 Homo sapiens cDNA clone G50D1075922 5
 prime, mRNA sequence.
 VERSION AL553407
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 950)
 AUTHORS Li, W.-B., Gruber, C., Jessup, J. and Polyzos, P.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope Centre National de Sequencage

HP 191 91006, EVRY cedex - France
 Email: seqrot@genoscope.cns.fr, web: www.genoscope.cns.fr.
 Location/Qualifiers
 1. 950
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 /db_xref="taxon:9606"
 /clone="G50D1075922"
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 /note="Vector: pCMVSPORT 6; Site: 1. Not: 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double stranded cDNA was digested with Not I and
 cloned into the Not I and Eco RV sites of the pCMVSPORT 6
 vector. Library was normalized. Library was constructed by
 Life Technologies. Contact: Evry iland Life Technologies,
 Rockville, Maryland 20850, USA Fax: (1) 301 610 8471
 Email: t11land@liferotech.com url:
 http://fulllength.liferotech.com"

FEATURES

Alignment Scores:
 Pred. No.: 1,576/92
 Score: 896.00
 Percent Similarity: 75.09%
 Best local Similarity: 59.71%
 Query Match: 57.18%
 DB: 9
 Gaps: 0

FASTA COUNT 220 3 254 3 207 9 268 2 others
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 120 CAATATGCAATCTTCT 179
 23 AspserAractlyleuouPhleuAspserTyrleuProthPhelIleleuThr 42
 DB TCTTCAATCTGAAAGGCTTTGATGATGAAATCATATGCTTTTGGACAAATATGTTGG 239
 180 TCTTCAATCTGAAAGGCTTTGATGATGAAATCATATGCTTTTGGACAAATATGTTGG 239
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 DB TCTTCAATCTGAAAGGCTTTGATGATGAAATCATATGCTTTTGGACAAATATGTTGG 299
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 63 SerleuAractlyleuouPhleuTyrAsnLeuAlaIlePhleuLeuSerAlaTyrMet 82
 DB TCTTCAATCTGAAAGGCTTTGATGATGAAATCATATGCTTTTGGACAAATATGTTGG 359
 300 TCTTCAATCTGAAAGGCTTTGATGATGAAATCATATGCTTTTGGACAAATATGTTGG 359
 83 leuValGlnleuLysleuSerSerTTPGleuIlelylTyrAsnLeuIncysHisMet 102
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 103 AspserAlaGlyGlyAspValAractlyleuValleleuTPrTPrTyrTPrPse 122
 DB TCTTCAATCTGAAAGGCTTTGATGATGAAATCATATGCTTTTGGACAAATATGTTGG 478
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 123 LysleuValGlnleuPseuLleTPrleuGlyAsnLysTyrMetLysAsnPrPAlaLeu 142
 DB TCTTCAATCTGAAAGGCTTTGATGATGAAATCATATGCTTTTGGACAAATATGTTGG 538
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 659 TCTTCAATCTGAAAGGCTTTGATGATGAAATCATATGCTTTTGGACAAATATGTTGG 718
 203 LysTyrleuThrGlnAlaGlnLeuValGlnPh-VallleuThrIleThrHisThrLeuSer 222

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D) 719 AAGTACATCATCAGCGGACCTGCTTACGTTGTCGACAAATCATCCAGCAGCGC 778
Q* 223 AlaValValysProGlyPheProPheGlyGlySLeuLeuPheGlySerSerTyrMet 242
D) 779 GGGGTCACTGCGCGACATTCCTCTGCTGTC-GTTGTAATTCACATTGATACATG 837
Q* 243 MetThrLeuValLeuLeuPheLeuAsnPheTyrTleGlnThrTyrArgLys-LysProVa 262
D) 838 ATTCCCTATTCTCTCTTCACAAACTTCATCATTCACCTACACACAGAAAGGGCT 897
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RESULT 14
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DEFINITION AL514872 L11.N1006.PL2 Homo sapiens cDNA clone Cl0BB01.42F12.5
ACCESSION AL514872 GI:12778365
VERSION AL514872.1 GI:12778365
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 861)
AUTHORS Li,W.B., Gruber,C., Jesse,J. and Polayes,D
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr Web: www.genoscope.cns.fr

FEATURES
Source
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/tissue_type="placenta"
/note="Vector: pCMVSPORT 6, Site: NotI, 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
Email: fliang@lifestech.com URL:
http://fulllength.invitrogen.com"

BASE COUNT 193 a 232 c 180 g 256 t
ORIGIN
Alignment Scores:
Pred. No.: 1..49e-91 Length: 861
Score: 887.00 Matches: 155
Percent Similarity: 76.19% Conservative: 37
Best Local Similarity: 61.51% Mismatches: 60
Query Match: 56.60% Indels: 1
DB: 9 Gaps: 0

US-09-624-670-63 (1-292) x AL514872 (1-861)
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D) 105 CAATATGACATTTTATGATCATCATCTTACTACTATTTTCAAGCATTCCTAGGCCCTGCA 164
QY 23 AspSerArgValArgGlyTyrPheLeuLeuAspSerTyrLeuProThrPheLeuThr 42
D) 165 GATACAGAGCTAAAGAGATGCTTCTCTGACAAATATATATACCACTTATCTGCTCT 224

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D) 225 GTCATATATTATATATATATATATATATATATATATATATATATATATATATATATAT 284
QY 63 SerLeuArgGlyTyrLeuThrLeuLysAsnLeuAlaThrLeuLeuSerAlaTyrMet 82
D) 285 TCTTGGCTGGGCGGATTTTACGTGGTAACTTCGACACACACACACACACACACACACAC 344
QY 83 LeuValGlnLeuLeuSerSerThrThrGlyGlyTyrAsnLeuGlnGlyGlnLeu 102
D) 345 TTCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 404
QY 103 AspSerAlaGlyCysCysValArgValAlaLysValLeuTyrTyrPheSer 122
D) 405 CGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 463
QY 123 LysLeuValGlnPheLeuAspThrThrPhePheValLeuGlnGlyLysThrAsnGlnLe 142
D) 464 AAGCTCATACAAATTTATGACACATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 523
QY 143 ThrPheLeuHisValTyrHisHisAlaSerMetPheAsnThrThrThrPheValLeuAsn 162
D) 524 AGGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 583
QY 163 ThrPheProGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyG 182
D) 584 TGGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 643
QY 183 MetTyrSerTyrTyrGlyLeuSerValPheProSerMetHisLysTyrLeuThrPheLys 202
D) 644 ATCTACCTTACATATGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 703
QY 203 LysTyrLeuThrThrAlaGlnLeuValGlnPheValLeuThrThrThrThrThrThrSer 222
D) 704 AATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 763
QY 223 AlaValValysProGlyPheProPheGlyGlySLeuLeuPheGlySerSerTyrMet 242
D) 764 GGGGTCACTGCGCGACATTCCTCTGCTGTC-GTTGTAATTCACATTGATACATG 824
QY 243 MetThrLeuValLeuLeuPheLeuAsnPheTyrTleGlnThrTyrArgLys-LysProVa 254
D) 824 ATTCCCTATTCTCTCTTCACAAACTTCATCATTCACCTACACACAGAAATGGCT 859

RESULT 15
LOCUS R0883263 847 bp mRNA linear EST_14-APR-2002
DEFINITION R0883263 AL514872 L11.N1006.PL2 Homo sapiens cDNA clone JMACB-7349766
ACCESSION R0883263 GI:122275271
VERSION R0883263.1 GI:122275271
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 847)
AUTHORS Li,W.B., Gruber,C., Jesse,J. and Polayes,D
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: rstraus@nsl.jhu.edu
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: Applied Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the T.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L10C2537 row: 1 column: 15
High quality sequence stop: 688.
Location/Qualifiers
1..897

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GenCore version 5.1.6
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OV protein - nucleic search, using frame_plus.p2n model

Run on: June 15, 2003, 21:11:36 : Search time 2216.45 Seconds
(without alignments)
3925.989 Million cell updates/sec

Title: US-09-624-670-64
Perfect score: 1651
Sequence: 1 MHPDASLSTYKAFKFLGPRD.... HTNSPSPLENSVPRPKPKU 299

Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:
-MODE=frame+2n-model -3V-x1p
-2/cg2.1/uspt0/us03624670/runat.11062003.075430.11630/app.query.fasta.1.910
-DB=GenEmbl -OPMT=fastap -SUPER=tree -MINMATCH=0.1 -LOOPC=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR=SCORE=pcr -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pro -NOR=ext -HEA=SIZE=500 -MINLEN=0 -MAXLEN=210000000
-USBR=US03624670.#CGN_1_1.3854.#runat.11062003.075430.11630 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEORDER -NFG_SCORES=0 -WAIT -DSPH=OCK=100 -J=NGILOG
-DEV_TIMEOUT=120 -MAPN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6
-Fgapext=7 -YGAPOP=10 -YGAPEXT=0.5 -DELop=6 -DELext=7

Database :
1: GenEmbl:*
2: gb_da:*
3: gb_hg:*
4: gb_in:*
5: gb_om:*
6: gb_ov:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_pr:*
11: gb_sts:*
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13: gb_un:*
14: gb_vt:*
15: em_da:*
16: em_hu:*
17: em_hu:*
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19: em_mu:*
20: em_om:*
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22: em_ov:*
23: em_pl:*
24: em_pl:*
25: em_pl:*
26: em_sts:*
27: em_sts:*
28: em_un:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	length	DB ID	Description
1	1651	100.0	900	6	AX464735
2	1647	99.8	2702	10	BC032911
3	1577	95.5	900	10	AB071985
4	1559	94.4	900	9	AF231981
5	1558	94.4	2257	9	HSMB01903
6	1558	94.4	3011	9	AF338241
7	1558	94.4	914	6	AX464732
8	1557	94.3	2592	6	105465
9	1557	94.3	2592	6	AF465620
10	1156	70.0	1397	5	AX127718
11	1148	69.5	925	6	AX464734
12	956.5	57.9	879	6	AF170608
13	956.5	57.9	3708	10	AF170608
14	956.5	57.9	3708	10	AF170608
15	956.5	57.9	3708	10	AF170608
16	669	40.5	2868	10	AF277093
17	653.5	39.6	945	6	AX464746
18	653.5	39.6	2219	9	AK055277
19	653.5	39.6	2000	9	AF277094
20	653.5	39.6	2000	9	AF277094
21	653.5	39.6	2000	9	AF277094
22	653.5	39.6	2000	9	AF277094
23	650.5	39.4	3072	9	AR063100
24	586	35.5	2485	14	AF198100
25	541.5	32.8	1986	3	AV119173
26	516	31.3	2065	3	AV119173
27	505	30.6	85794	5	AC055019
28	498	30.2	2580	3	AY060267
29	484	29.3	846	6	AX464749
30	476	28.9	1486	9	AC000618
31	474.5	28.7	1457	9	AK001653
32	474	28.7	1684	3	AY060447
33	472	28.6	1840	10	BC006602
34	471.5	28.6	949	6	AX052771
35	471.5	28.6	1471	9	AF336793
36	467	28.3	1471	9	AF336793
37	462.5	28.0	1137	10	BC006735
38	462.5	28.0	1484	10	AF170607
39	462.5	28.0	1484	10	AF170607
40	451	27.3	2508	9	AX052779
41	448	27.1	2091	17	AF11849
42	431.5	26.1	1595	3	AY061182
43	426	25.8	2018	3	AV117657
44	425.5	25.8	50374	2	AC015170
45	425.5	25.8	164193	4	AY064494

ALIGNMENTS

RESULT 1

US-09-624-670-64 (1-299) x BC022911 (1-2702)	
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Translation: "MEHFDASLTYFKALGPDRTRVKGWFLDNTPTFVCSVITLL IWLGRKYNKRPSPSCRGILQVNLGTLTLSTLYFELTVGWEGKYNFPCGSTRSA GESDMKIIIVLWMYFSKLIEMDFEFLIRKNHQTIVLHVHATMLIMFWVNM VPCGHSYFGATLNSFTHVLMVSYGLSPSMRBYLMWKVITDGOGLVOPVLIT CGVIMPCSPFLGMILFQIOLYMSLIALFTNFIOTYNNKSGASRRKHLKOHNGSVAA VNCHTNSPFLNSVSKPRKORD"	
BASE COUNT	710 a 607 c 577 g 808 t
ORIGIN	
Alignment Scores:	
Pred. No.:	8,32e-152
Score:	1647.00
Percent Similarity:	100.00%
Best Local Similarity:	99.67%
Query Match:	99.76%
DB:	10
Length:	2702
Matches:	298
Conservative:	1
Mismatches:	0
Indels:	0
Gaps:	0
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D3	80 ATGGACAAATTTCCATGGCTACTACTACTATTTCAAGCCCTTCTCGCCCGGACAT 139
Q7	21 ThrArgValIysGlyTrpPheLeuLeuAspAsnTyrlleProThrPheValCysSerVal 40
D3	140 ACAAGAGTCAAAGATGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 199
Q7	41 IletyrLeuLeuLeuValIleValIlePheGlyProLysTyrrMetLysAsnArgGlnProPheSer 60
D3	200 ATTACTACTACATTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 259
Q7	61 CysArgGlyIleLeuGlnLeuTyrrAsnLeuGlyLeuThrLeuLeuSerLeuTyrrMetPhe 80
D3	260 TGCCGAGGACATCTGCGAGTGTGATTAACCTTGACCTACCTGCTGCTGCTGCTGCT 319
Q7	81 TyrGluLeuValIleThrGlyValIleThrGlyLysTyrrAsnPhePheCysGlnIleThrArg 100
D3	320 TATGAGTGTGACAGGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 379
Q7	101 SerAlaGlyIleGluSerAspMetLysIleIleArgValLeuThrPrrTyrrPheSerLys 120
D3	380 ACCGCGGAGAAATCGATATGATGATGATGATGATGATGATGATGATGATGATGAT 439
Q7	121 LeuIleGluPheMetLysPhePhePheIleLeuArgLysAsnAsnHisGlnIleThr 140
D3	440 CTCATCGAATTCATGACACCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 499
Q7	141 ValLeuHisValIleThrHisHisAlaThrMetLeuAsnIleThrPrrPheValMetAsnTrp 160
D3	500 GTGCTCATGCTGCTACACACGCTACCATGCTCAACATCTGGTGTGGTGTGGTGTGG 559
Q7	161 ValProGlyGlyHisSerTyrrPheGlyAlaThrLeuAsnSerPheIleHisValLeuMet 180
D3	560 GTTCCCTGGGCGCATTCATTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 619
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Q7 261 ArgArgLysAspHisLeuLysGlyHisIleGlnGlySerValAlaAlaValAsnGlyHis 280

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Q7 281 ThrAsnSerPheProSerLeuGluAsnSerValIlePheArgLysGlnArgLysAsp 299

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RESULT 3

AB071985

LOCUS

DEFINITION

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Db	180 ACTAGAGTAAAAAGCACGCTTCCTTCGACAAATAATAdGCCATTTATCTCTCTTCG 239
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REFERENCE 1 Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo.
AUTHORS Mokerji, P., Das, T., Huang, Y.S., Parker-Barnes, J.M., Leonard, A.E.,
Thurnmond, J. and Perrella, S.L.
TITLE Elongase genes and uses thereof
JOURNAL Patent: WO 0206401-A 3 31-JAN-2002;
Abbott Laboratories (US)
FEATURES location/Qualifiers
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US-09-624-670-64 (1-299) x AX464732 (1-914)

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ACCESSION 105465 GI:590717
VERSION 105465.1
KEYWORDS
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ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2592)
AUTHORS Ishizaka, K., Martens, C.L. and Moore, K.W.
TITLE Glycosylation inhibition factors
JOURNAL Patent: EP 0285405-A1 1 05-OCT-1988;
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US-09-624-670-64 (1-299) x 105465 (1-2592)

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QY      241 SerLeuIleAlaSerPheThrAsnPheTrpIleGlnIleTrpAsnLysGlyAlaSer 260
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AX052773
VERSION
AX052773.1 GI:12226935
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REFERENCE
Jacobson, A.T., Asadi, A.T., Westberg, P.T., Nedergaard, J.T., and
Tyrdyk, P.M.
Fatty acid elongation genes and uses thereof
Patent: WO 00/0945-A 5 (40-NV-2000);
Karolinska Innovations AB (SE)
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DB      106 TCTGCAATTCGCGTGGTGGTCTGCGACTCTTACCTCCGCACTTATCTTACCATC 165
QY      41 lletYrleuLeuValItrPheGlyProLysTyrmelLysAsnArgGlnProPheSer 60
DB      166 ACGTACCTCCTCGATATGCGTGGTAAACATGACATGACAGAGCGCTCCTCTCT 225
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Search completed: June 15, 2003, 23:02:03
Job time : 2225.45 secs



GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 15, 2004, 20:25:36 : Search time 206.416 Seconds
(without alignments)
3262 086 Million cell updates/sec

Title: US-09-624-670-64

Perfect score: 1651
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Searched: 2145233 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	1556	94.4	2001	23	Human prostate exp
7	1556	94.4	2313	21	Human prostate asso
8	1556	94.4	2627	22	Human full-length
9	1556	94.4	2769	22	Human full-length
10	1556	94.4	3083	22	Human contig polyn
11	1556	94.4	914	24	Human elongase HSE
12	1555	94.2	2710	21	Breast cancer prot
13	1489.5	90.2	2571	9	Fragment from clon
14	1343	81.3	1997	24	Human polynucleoti
15	1148	69.5	975	22	Human cold-induced
16	1108	67.1	871	22	CDNA encoding nove
17	1085	65.7	680	22	Human cDNA 5'-end
18	1085	65.7	680	22	Human cDNA clone r
19	1069	64.7	748	22	CDNA encoding nove
20	956.5	57.9	879	24	Mouse elongase MEL
21	956.5	57.9	3795	22	Mouse fatty acid e
22	956	57.8	817	22	Human cDNA clone r
23	954.5	57.8	3645	23	Human prostate exp
24	954.5	57.8	3645	23	Human prostate exp
25	954.5	57.8	3645	23	Human prostate exp
26	772	46.8	809	22	Human neuroblastom
27	753	45.8	795	22	Human cDNA clone r
28	753	45.8	927	22	Human neuroblastom
29	724	43.9	1225	21	Human cancer assoc
30	669	40.5	1292	21	Mouse elongation o
31	654.5	39.6	972	24	Human elongation o
32	653.5	39.6	1203	23	CDNA encoding nove
33	653.5	39.6	3383	24	Human MDDT encodin
34	653.5	39.6	3415	24	Human cDNA encodin
35	624.5	37.8	493	24	Human colon cancer
36	624.5	37.8	967	24	Human elongation o
37	598	36.2	874	22	Human cDNA 5'-end
38	598	36.2	874	22	Human cDNA clone r
39	598	36.2	1090	22	Human full-length
40	579	35.1	488	23	CDNA encoding nove
41	559	33.9	404	23	Human prostate exp
42	559	33.9	598	23	Human prostate exp
43	526	31.9	423	23	Human prostate exp
44	526	31.9	363	23	Human prostate exp
45	504	30.5	1914	23	Drosophila melanog

ALIGNMENTS

RESULT 1
ABK46370
ID ABK46370 standard. cDNA; 900 BP.

AC ABK46370;

XX 05-JUN-2002 (first entry)

XX Mouse elongase MELO? cDNA.

XX ss, gene, elongase, polyunsaturated fatty acid, pufa; transgenic plant;
XX transgenic non human animal; plant oil, arachidonic acid, nutritional;
XX pharmacological, cosmetic, animal feed, rickettsia; angioptasia, AIDS,
XX acquired immunodeficiency syndrome; multiple sclerosis; cachexia, asthma;
XX inflammatory skin disease; osteoporosis; kidney stone, cancer; eczema;
XX inflammation; rheumatoid arthritis; psoriasis; platelet aggregation;
XX vasodilation; cholesterol reduction; gastrointestinal bleeding.

OS Mus sp.
 PN W020208421 A2.
 XX
 PD 41-JAN 2002.
 XX
 PF 24-JUL-2001: 2001W0 US24259.
 XX
 PR 24-JUL-2000: 2000US 0624670.
 PR 11-JUL-2001: 2001US 0903456.
 XX
 PA (ABHO) ABHOFT LAB.
 PI Mukerji P., Das I., Huang Y., Parker-Barnes JM., Leonard AF.
 PI Thurmond J., Pereira SL.
 XX
 DR WPI: 2002.17201722.
 DR P-PSDB: AA087834.
 XX
 PT Isolated nucleic acid sequences encoding elongase proteins, useful in
 PT the production of polyunsaturated fatty acids, e.g. arachidonic acid,
 PT which can then be used nutritional compositions and pharmaceutical
 PT compositions (for treatment AIDS).
 XX
 PS Claim 8; Fig 58; 27pp; English
 XX
 CC The invention relates to isolated nucleic acid sequences encoding
 CC elongase proteins and the elongase proteins themselves. Also
 CC included are a purified polypeptide which elongates polyunsaturated
 CC fatty acids and has at least 30% amino acid similarity to the amino acid
 CC sequence to an elongase protein, a vector comprising the nucleic
 CC acid, a plant cell (or tissue or whole plant) comprising the vector and
 CC expressing the nucleic acid, a plant oil or acid expressed by the
 CC transgenic plant, and a transgenic non-human animal expressing elongase
 CC in its fluid. The nucleic acids and elongase proteins may be used
 CC directly or indirectly in the production of polyunsaturated fatty acids
 CC (pufa), for e.g. arachidonic acid, which can then be used nutritional
 CC compositions, pharmaceutical compositions, cosmetics and animal feeds.
 CC The pharmaceutical compositions may be used in the treatment of
 CC restenosis after angioplasty, AIDS (acquired immunodeficiency syndrome),
 CC multiple sclerosis, inflammatory skin diseases, osteoporosis, kidney or
 CC urinary tract stones, malignant cancer, cachexia associated with cancer,
 CC eczema, symptoms of inflammation, rheumatoid arthritis, asthma and
 CC psoriasis, they are also useful for inhibiting platelet aggregation,
 CC inducing vasodilation, reducing cholesterol, reducing or preventing
 CC gastrointestinal bleeding and side effects of non-steroidal
 CC anti-inflammatory drugs. The present sequence encodes an elongase
 CC of the invention.
 XX
 SQ Sequence 909 BP: 299 A: 256 G: 200 C: 235 T: 0 other.
 XX
 Alignment Scores:
 Pred. No.: 5,57e 171 Length: 900
 Score: 1651.00 Matches: 299
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 24 Gaps: 0
 US 09-624 670 64 (1-299) x 484,670 (1-900)
 QY 1 MotGluHisPheAspAlaSerLeuSerThrTyrPheGlySalPheGluGlyProArgAsp 20
 DB 1 ATGGAAATTTGATGATGTCACACAGTACTATTTCAAGAGCTTCCTGGAGGAGGAGAT 60
 QY 21 ThrArgValGlySerTyrPhePheGluGluAsnTyrIleThrThrPheValCysSerVal 40
 DB 1 ACAAGAGTCAAGAGATGATGTCCTCGGACAAATATACCTTACCTTACCTTGTCTGT 120
 QY 41 IleTyrLeuLeuIleValTrpLeuGlyProGlySerTyrMetHisAsnAspPropheSer 60
 DB 121 ATTACTACTCACTGATGATGATGAGGATCAAAATATATGAAGAACCTGCTACCTTCT 180
 QY 61 CysArGlyTleLeuGlnLeuTyrAsnGluGlyLeuThrLeuGluSerLeuTyrMetPhe 80
 DB 161 TGGGAGAGATGAGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 240
 QY 81 TyrGluLeuValThrGlyValTrpGluGlySerTyrAsnGluGlyCysGlnGlyThrArg 100
 DB 241 ATACAGTTGGTGAAGAGTGGGAGAGGAAAATAAAATATTTTCTGCTAAAGCAACAGC 300
 QY 101 SerAlaGlyGluSerAspMetLysIleIleArgValLeuTyrTrpTyrTyrPheSerLys 120
 DB 301 AGGAGGAGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 460
 QY 121 LeuIleGluPheMetAspThrPhePhePheIleLeuArgGlySerAsnGluIleThr 140
 DB 361 CTATGCAATTCATGACACCTTTTCTTCATGCTTTCGAAAGAAATATATTTTCTTCC 420
 QY 141 ValLeuHisValTyrHisHisAlaThrMetLeuAsnIleTyrTrpPheValMetAsnTrp 160
 DB 421 GTGCTCATGCTTACCAACCACTACCACTACCACTACCACTACCACTACCACTACCA 480
 QY 161 ValProCysGlyHisSerTyrPheGlyAlaThrLeuAsnSerPheIleHisValLeuMet 180
 DB 481 GTTCAATGAGGAGATGATATTTTGGTGGAGACATTAACAGATTATCATGCTCTCAT 540
 QY 181 TyrSerTyrTyrGlyLeuSerSerIleThrSerMetArgPheTyrIleThrTrpPheLys 200
 DB 541 TACTGCTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
 QY 201 TyrIleThrGluGlyGlnLeuValGlnPheValLeuThrIleIleGlnThrThrCysGly 220
 DB 601 TACATCACTCAAGGAGCTGGGCCAGTTTGTGTCGCAATGATGACAGACGATGCGCG 660
 QY 221 ValPheTrpProGlySerPheProLeuGlyTyrPheGluGlyIleGlyTyrMetIle 240
 DB 661 GTCTTCTGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
 QY 241 SerLeuIleAlaIlePheThrAsnPheTyrIleGlnIleThrTyrAsnLysLysGlyAlaSer 260
 DB 721 TGGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
 QY 261 ArgArgTyrAspHisLeuGlyHisGlnAsnGlySerValAlaIleValAsnGlyHis 280
 DB 781 CGGAGCAAGACCACTGAGAGGAGCACTAAGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
 QY 281 ThrAsnSerPheProSerLeuGluAsnSerValLysProArgLysGlnArgLysAsp 299
 DB 841 ACCAAGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 897
 RESULT 2
 AA294241
 ID AA294241 standard; cDNA 914 BP.
 XX
 AC AA294241;
 XX
 DT 03-JUL-2000 (first entry)
 XX
 DE Human elongase HSELO1 cDNA.
 XX
 KW Elongase; HSELO1; polyunsaturated fatty acid; adipic acid;
 KW dihydro gamma linolenic acid; cyclooctatetraenoic acid;
 KW transgenic plant; transgenic animal; human; ss.
 OS Homo sapiens.
 XX
 PN W0200012720 A2.
 XX
 PD 09-MAR-2000.
 XX
 PF 30-AUG-1999: 99MO-US14715.
 XX
 PR 02-SEP-1998: 98US-0145428.
 XX
 PA (ABHO) ABHOFT LAB.

XX Mukerji P, Leonard AE, Huang Y, Thurmond J, Kirchner SJ;
 PI Parker-Barnes JM, Das T;
 XX WPI: 2000-237881/20.
 DR P-PSDB: AAY83932.
 XX
 PI Isolated nucleic acids encoding elongase enzymes for producing
 PT polyunsaturated fatty acids that can be used to form nutritional
 PT compositions -
 XX Claim 114; Fig 43; 210pp; English.
 XX This sequence is the coding region of cDNA encoding a human
 CC elongase, termed HSELO1 (see AAY79244). The cDNA was isolated from a
 CC human liver cDNA library by PCR amplification (see AAY24253-54).
 CC HSELO1 is involved in the elongation of polyunsaturated fatty acids
 CC (PUFAs). It is capable of catalysing the conversion of
 CC gamma-linolenic acid, stearidonic acid and arachidonic acid to
 CC dihomogamma-linolenic acid, eicosatetraenoic acid and adrenic acid,
 CC respectively. The invention provides M. alpina, human and
 CC Caenorhabditis elegans elongase nucleotide sequences (see AAY94239-41)
 CC and proteins, vectors comprising nucleotide sequences, eukaryotic
 CC and prokaryotic host cells, plant cells, plants or plant tissues
 CC comprising such vectors, transgenic non-human mammals whose genome
 CC comprises a nucleotide sequence encoding an elongase, a method for
 CC producing a PUFA using a host cell expressing an elongase, and
 CC nutritional, pharmaceutical, cosmetic and animal feed compositions
 CC comprising the PUFA.
 XX
 SQ Sequence 914 BP; 237 A, 223 C, 199 G; 255 T; 0 other;

Alignment Scores:
 Pred. No.: 6,69e-161 Length: 914
 Score: 1559,00 Matches: 278
 Percent Similarity: 97.32% Conservative: 13
 Best Local Similarity: 92.98% Mismatches: 8
 Query Match: 94.43% Indels: 0
 DB: 21 Gaps: 0

US-09-624 670-64 (1-299) x AAY94241 (1-914)

QY 1 MetGluHisPheAspAlaSerLeuSerThrTyrPheLysAlaPheLeuGlyProArgAsp 20
 DB 1 ATGGACATTTTGATGTCATATCTAGTACCTATTTCAGGACATTGCTAGGCGCTCGAGAT 60
 QY 21 ThrArgValLysGlyTyrPheLeuLeuAspAsnTyrIlePheThrPheValCysSerVal 40
 DB 61 ACTAGAGTAAAGCAAGGATGCTCTCTGACAAATATATACCCACATTTATCTCTCTGTC 120
 QY 41 IleTyrLeuLeuIleValTrpLeuGlyProLysTyrMetLysAsnArgGlnProPheSer 60
 DB 121 ATATATTACATAATTTGATGCTGGACCAATATACATGAGGAATAAACAGCATTCCTC 180
 QY 61 CysArgGlyIleLeuGlnLeuTyrAsnLeuGlyLeuThrLeuLeuSerLeuTyrMetPhe 80
 DB 181 TGCAGGAGGATTTTATAGTGGTATTAACCTTGGACTCACACTGCTGCTGTATATGTC 240
 QY 81 TyrGluLeuValThrGlyValTrpGluGlyLysTyrAsnPheCysGlnGlyThrArg 100
 DB 241 TGTGAGTTAGTAACAGGAGTATGGCAAGGCAAAATACAACTTCTTCTGTCAGGGCACCG 300
 QY 101 SerAlaGlyGluSerAspMetLysIleIleArgValLeuTrpTrpTyrTyrPheSerLys 120
 DB 301 ACCGAGGAGAGATCAGATATGAAGATTTATCGTGTCTCTGTGTGTACTACTTCTCCAAA 360
 QY 121 LeuIleGluPheMetAspThrPhePheIleLeuArgLysAsnAsnHisGlnIleThr 140
 DB 361 CTCATAGATTTATGAAATTTTCTTCTTCTATCTGCTGCGCAAGAAACACACAGATCAG 420
 QY 141 ValLeuHisValTyrHisHisAlaThrMetLeuAsnIleTrpTrpPheValMetAsnTrp 160
 DB 421 GTCTCTGACGCTACACCAATGCCCTCCGATCTGCTGACATCTGCTGTGTGTGTGATGA 480

QY 161 ValProCysGlyHisSerTyrPheGlyAlaThrLeuAsnSerPheIleHisValLeuMet 180
 DB 481 GTCCCTGCGCCACCTCTTATTTTGGTGCACACTTAATAGCTTCATCCAGTCTCCTCATG 540
 QY 181 TTTSerTyrTyrGlyLeuSerSerIleProSerMetArgProTyrTyrLeuTrpIleLys 200
 DB 541 TACTCTTACTATGTTTGTGTCAGTCCCTTCCATCGTCCATACCTCTGTGGTGAAGAAG 600
 QY 201 TyrIleThrGlnGlyGlnLeuValGlnPheValLeuThrIleIleLeuThrThrCysGly 220
 DB 601 TACATCACTCAGGGGAGCTGCTTCACTTGTCTGACAAATCATCCAGACAGCTCGGG 660
 QY 221 ValPheTrpProCysSerPhePheProLeuGlyTyrPhePheGlnIleGlyTyrMetIle 240
 DB 661 GTCATCTGGCGGTGCACATTCCTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720
 QY 241 SerLeuIleAlaLeuPheThrAsnPheTyrIleGlnThrTyrAsnLysLysGlyAlaSer 260
 DB 721 TCCCTGATGCTCTCTTTCACAACTTCTACATTCACACCTACACAAAGAAAGGGCTCC 780
 QY 261 ArgIleLysAspHisLeuLysGlyHisGlnAsnGlySerValAlaAlaValAsnGlyHis 280
 DB 781 CGAAGGAAAGACACCTGGAAGGACCCAGCAATGGGTCCATGCTCTGTGTGTGTGTGT 840
 QY 281 ThrAsnSerPheProSerLeuGluAsnSerValLysProArgLysGlnArgLysAsp 299
 DB 841 ACCAACAGCTTTTTCACCCCTGGAAGAAACATGTGAAGCCAAAGGAAGCTCGGAAGGAT 897

RESULT 3
 ABV23421
 ID ABV23421 standard; cDNA; 2001 BP.
 XX AC ABV23421;
 XX DT 16-SEP-2002 (first entry)
 XX DE Human prostate expression marker cDNA 23412.
 XX KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 XX OS Homo sapiens.
 XX PN WO200150860-A2.
 XX PD 23-NOV-2001.
 XX PF 20-FEB-2001; 2001WO-US05171.
 XX PR 17-FEB-2000; 2000US-183319P.
 XX PR 16-MAR-2000; 2000US-189862P.
 XX PR 25-MAY-2000; 2000US-207454P.
 XX PR 19-JUN-2000; 2000US-211314P.
 XX PR 18-JUL-2000; 2000US-216007P.
 XX PR 13-DEC-2000; 2000US-255281P.
 XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX PI Schlegel R, Endege WO, Monahan JE;
 XX DR WPI: 2001-662795/76.
 XX Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer -
 XX Claim 1; Page 4265-4266; 11750pp; English.
 XX The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification or its complement. (I) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;

CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
 XX
 SQ Sequence 2001 BP; 527 A; 581 C; 399 G; 489 T; 5 other;
 Alignment Scores:
 Pred. No.: 2,026 160 Length: 2001
 Score: 1559.00 Matches: 278
 Percent Similarity: 97.32% Conservatives: 13
 Best local Similarity: 92.98% Mismatches: 8
 Query Match: 94.43% Indels: 0
 DB: 23 Gaps: 0
 US: 09-624-670-64 (1-299) x ABV: 2421 (1-2001)
 QY 1 MetGluHisPheAspAlaSerLeuSerThrTyrPheHisAlaPheLeuGlyProArgAsp 20
 DB 177 ATGGAACTTTTATGTCATCATCTTATATATATATATATATATATATATATATATAT 46
 QY 21 ThrArgValIleGlyTyrPheLeuLeuAspAspTyrIleProThrPheValCysSerVal 40
 DB 237 ACTACAGTAAAG 296
 QY 41 IleTyrLeuLeuValIlePheLeuLeuValPheProLysTyrMetLysAsnArgGlnProPheSer 60
 DB 297 ATATATTATATATTTGATGCTGGACCAAAAATAATAGAGAAATAAATAGCAATCTCT 456
 QY 61 CysArgGlyIleLeuGlnLeuTyrAsnLeuGlyLeuThrLeuLeuSerLeuTyrMetPhe 80
 DB 357 TGCCGGGGGATTTTAGTGATGATATATATATATATATATATATATATATATATATAT 416
 QY 81 TyrGluLeuValIleHisGlyValIlePheGlyLysTyrAsnIlePheCysGlnIleThr 100
 DB 417 TGTGAGTTAGTAACAGAGATGGGAGGCAATATACAACTCTCTGTCAGGGCACCG 476
 QY 101 SerAlaGlyHisSerAspMetLysIleLeuValLeuThrTyrTyrPheSerLys 120
 DB 477 ACCGCAAGCAAT 546
 QY 121 LeuIleGluPheMetAspThrPhePhePheLeuAlaGlyAsnAsnHisGlnIleThr 140
 DB 537 CTCATCAATTTATGGACATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 596
 QY 141 ValLeuIleValTyrHisHisAlaThrMetLeuAsnIleTrpTrpPheValMetAsnTrp 160
 DB 597 GTCTGCACTCTACCAATACGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 656
 QY 161 ValProCysGlyHisSerTyrPheGlyAlaThrLeuAsnSerPheTyrLeuValLeuMet 180
 DB 657 GTCCCTGGGAGCACTTTATTTTGTGGCACTTATATAGTTTATATATATATATATATAT 716
 QY 181 TyrSerTyrGlyHisSerTyrPheSerMetTyrPheTrpTrpTrpTrpTrpTrpTrp 200
 DB 717 TACTTCTATGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 776
 QY 201 TyrIleThrGlnGlyHisLeuValGlyPheValLeuThrIleLeuGlnThrTyrCysGly 220
 DB 777 TACATCACTACGGGAGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 836
 QY 221 ValPheTrpPheCysSerPhePheGlyTyrLeuPhePheCysIleIleTyrMetIle 240
 DB 837 GTATCTGAGTGGCAATTCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 896
 QY 241 SerLeuIleAlaLeuThrAsnPheTyrIleGlnThrTyrAsnIleLysCysGlyAlaSer 260

DB 897 TGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 956
 QY 261 ArgArgLysAspHisLeuGlyHisHisHisHisHisHisHisHisHisHisHisHisHis 280
 DB 957 CGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 1016
 QY 281 ThrAsnSerPhePhePhePhePhePhePhePhePhePhePhePhePhePhePhePhe 299
 DB 1017 ACCAACAGCTTTTACGCTGGGAAAATATGTGAAATCAAGGAAATGTGGGAAGGAT 1074
 RESULT 4
 ABV24778
 ID ABV24778 Standard; cDNA; 2001 BP.
 AC ABV24778;
 IT 16 SEP 2002 (first entry)
 XX Human prostate expression marker cDNA 24769.
 XX Human prostate expression marker cDNA 24769.
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 OS Homo sapiens.
 DN W0200160860-A2.
 XX W0200160860-A2.
 PD 23-AUG-2001.
 XX 20 FEB 2001; 2001WO-US05171.
 XX 17-FEB-2000; 2000US-18319P.
 PR 16-MAR-2000; 2000US-189862P.
 PR 25-MAY-2000; 2000US-207454P.
 PR 09 JUN 2000; 2000US-211314P.
 PR 18 JUN-2000; 2000US-219007P.
 PR 13-DEC-2000; 2000US-255281P.
 XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX Schlegel R, Endege WO, Monahan JR;
 XX WPI: 2001-662795/76.
 PT Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer
 PT
 PT Claim 1; Page 4740-4741-11750pp; English.
 XX The invention relates to an isolated nucleic acid molecule (1) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62214) of the
 CC specification or its complement. (1) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
 SQ Sequence 2001 BP; 527 A; 581 C; 399 G; 489 T; 5 other;
 Alignment Scores:
 Pred. No.: 2,026 160 Length: 2001
 Score: 1559.00 Matches: 278
 Percent Similarity: 97.32% Conservatives: 13

Best Local Similarity: 92.98% Mismatches: 8
 Query Match: 94.43% Indels: 0
 DB: 23 Gaps: 0

US-09-624-670-64 (1-299) x ABV24778 (1-2001)

QY 1 MetGluHisPheAspAlaSerLeuSerThrTyrPheLysAlaPheLeuGlyProArgAsp 20
 DB 177 ATGGAACATTTCATGATGATATCTAGTACCTATTTCAGGCATGCTAGGCTCGAGAT 236
 QY 21 ThrArgValLysGlyTyrPheLeuLeuAspAsnTyrIleProThrPheValCysSerVal 40
 DB 237 ACTAGAGTAAAGGATGCTTTCTCTGGACAATTATATACCCACATTTATCTGCTGTC 296
 QY 41 IleTyrLeuLeuIleValTyrPheLeuLeuAspAsnTyrIleProThrPheValCysSerVal 40
 DB 237 ACTAGAGTAAAGGATGCTTTCTCTGGACAATTATATACCCACATTTATCTGCTGTC 296
 QY 41 IleTyrLeuLeuIleValTyrPheLeuLeuAspAsnTyrIleProThrPheValCysSerVal 40
 DB 297 ATATATTTACTAATTTGTATGCTGGACCAAAATACATGAGGAATAAACACCATCTCT 356

RESULT 5
 ABV25364
 ID ABV25364
 AC ABV25364:
 XX
 XX
 DT 16-SEP-2002 (first entry)

Human prostate expression marker cDNA 25355.
 Human; prostate cancer; cytostatic; carcinogen, pharmacodynamic marker,
 pharmacogenomic marker; gene; ss.
 Homo sapiens.
 WC200160860-A2.
 23-AUG-2001.
 20-FEB-2001; 2001WO-US05171.
 17-FEB-2000; 2000US-183319P.
 16-MAR-2000; 2000US-189862P.
 25-MAY-2000; 2000US-207454P.
 09-JUN-2000; 2000US-211314P.
 18-JUL-2000; 2000US-216007P.
 13-DEC-2000; 2000US-255281P.
 (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Schlegel R, Endege WO, Monahan JE;
 WPI; 2001-662795/76.
 Novel isolated nucleic acid molecule associated with cancerous state of
 prostate cells and correlating with presence of prostate cancer, useful
 for detecting presence of prostate cancer, stage of prostate cancer -
 Claim 1; Page 5005-5006; 11750pp; English.
 The invention relates to an isolated nucleic acid molecule (I) comprising
 a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 specification or its complement. (I) is useful for:
 (a) assessing whether a patient is afflicted with prostate cancer;
 (b) monitoring the progression of prostate cancer in a patient;
 (c) assessing the efficacy of a test compound to inhibit prostate
 cancer in a patient;
 (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 in a patient;
 (e) selecting a composition for inhibiting prostate cancer in a patient;
 (f) assessing the prostate cell carcinogenic potential of a compound;
 (g) determining whether prostate cancer has metastasized in a patient;
 (h) assessing the aggressiveness or indolence of prostate cancer in a
 patient;
 (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
 Sequence 2001 BP; 527 A; 581 C; 399 G; 489 T; 5 other;

Alignment Scores:
 Pred. No.: 2,02e-160 Length: 2001
 Score: 1559.00 Matches: 278
 Percent Similarity: 97.32% Conservative: 13
 Best Local Similarity: 92.98% Mismatches: 8
 Query Match: 94.43% Indels: 0
 DB: 23 Gaps: 0

US-09-624-670-64 (1-299) x ABV25364 (1-2001)

QY 1 MetGluHisPheAspAlaSerLeuSerThrTyrPheLysAlaPheLeuGlyProArgAsp 20
 DB 177 ATGGAACATTTCATGATGATATCTAGTACCTATTTCAGGCATGCTAGGCTCGAGAT 236
 QY 21 ThrArgValLysGlyTyrPheLeuLeuAspAsnTyrIleProThrPheValCysSerVal 40
 DB 237 ACTAGAGTAAAGGATGCTTTCTCTGGACAATTATATACCCACATTTATCTGCTGTC 296
 QY 41 IleTyrLeuLeuIleValTyrPheLeuLeuAspAsnTyrIleProThrPheValCysSerVal 40
 DB 297 ATATATTTACTAATTTGTATGCTGGACCAAAATACATGAGGAATAAACACCATCTCT 356

XX DE Human full-length polynucleotide sequence #172.
 XX KW Mammal; human; rhesus monkey; baker's yeast; fission yeast; Norway rat;
 XX KW mouse; Chinese hamster; African clawed frog; fruit fly; dog; leukaemia;
 XX KW cancer; lymphoma; neuroblastoma; autoimmune disorder; cell proliferation;
 XX KW nervous system disorder; inflammatory disorder; cell differentiation; ds;
 XX KW aneuploidy; stem cell growth factor; activin; inhibin; cartilage; burn;
 XX KW genetic disorder; bone regeneration; tendon; ligament; tissue repair;
 XX KW cytostatic; antineoplastic; antiarthritic; vulnery; antiinflammatory;
 XX KW antibacterial; immunosuppressive; vasotropic; antiparkinsonian;
 XX KW neuroprotective; osteopathic; antidiabetic; antiallergic;
 XX KW immunostimulant; analgesic; gene therapy.
 XX OS Homo sapiens.
 XX PN WO200164834-A2.
 XX PD 07-SEP-2001
 XX PF 26-FEB-2001; 2003WO US04926.
 XX PR 28-FEB-2000; 2000US 0515126.
 XX PR 18-MAY-2000; 2000US-0577409.
 XX PR 17-JUN-2000; 2000US-0597707.
 XX PR 14-JUL-2000; 2000US-0616807.
 XX PR 19-SEP-2000; 2000US 0664641.
 XX PR (HYSK-) HYSEQ INC.
 XX PI Tanq YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
 XX PI Xue AL, Yang Y, Wehrman T, Wang J, Ma Y, Wang D, Chen R, Xu C;
 XX PI Brmanac R;
 XX PI WPI: 2001-589862/66.
 XX PR P-PSDB: AAU27847.
 XX FT Novel polypeptides and nucleic acids obtained from cDNA libraries
 XX FT prepared from various human tissues, for diagnosis, treatment of
 XX FT cancer, neurological, inflammatory disorders and for use in arrays for
 XX FT detection -
 XX PS Claim 1, SEQ ID NO 172, 153pp, English.
 XX CC Sequences AAS44576-AAS44919 represent full-length polynucleotides and
 XX CC contig polynucleotides encoding polypeptides of the invention. The DNA
 XX CC and protein sequences are useful for the treatment, diagnosis and
 XX CC prevention of various types of disorder in a mammalian subject such as a
 XX CC human, dog, monkey, mouse, hamster or rat. The disorders include cancers
 XX CC such as leukaemia, lymphoma and neuroblastoma, autoimmune disorders such
 XX CC as multiple sclerosis, connective tissue disease, rheumatoid arthritis,
 XX CC diabetes mellitus, allergic rhinitis, asthma and eczema, nervous system
 XX CC disorders such as parkinson's disease, Alzheimer's disease, Huntington's
 XX CC chorea, amyotrophic lateral sclerosis, spinal muscular atrophy and
 XX CC Wernicke disease, inflammatory disorders such as hepatitis, Crohn's
 XX CC disease, ischaemia-reperfusion injury, shock, sepsis and inflammatory
 XX CC bowel disease. The sequences exhibit activity relating to angiogenesis,
 XX CC cell proliferation, cell differentiation, stem cell growth factor,
 XX CC activin or inhibin. Therefore, they can be used to manipulate stem cells
 XX CC in culture to give rise to neuroepithelial cells that can be used to
 XX CC augment or replace cells damaged by illness, accidental damage or genetic
 XX CC disorders. The sequences may also be used for regeneration of bone,
 XX CC cartilage, tendons and ligaments and in tissue repair and burn healing.
 XX CC Note. Some sequences for this patent did not form part of the printed
 XX CC specification, but were obtained in electronic format directly from Wipo
 XX CC at http://wipo.int/pub/published_pct_sequences.
 XX SQ Sequence 276a BP, 799 A, 543 C, 554 G, 873 T, 0 other;
 XX AAS44919
 XX ID AAS44919 standard; DNA; 3083 BP.
 XX XX
 XX AC AAS44915;
 XX XX
 XX DT 18-DEC-2001 (first entry)

Best Local Similarity: 92.98% Mismatches: 8
 Query Match: 94.43% Indels: 0
 DB: 22 Gaps: 0
 US-09-624-670-64 (1-299) X AAS44747 (1-2769)
 QY 1 MetGluHisPheAspAlaSerLeuSerThrTyrPheLysAlaPheLeuGlyProArgAsp 20
 DB 136 ATGGAAATTTTGGATGATCATCACTTAACTACCTTTCAGAGCATTTGCTAGGCCCTCGAGAT 195
 QY 21 ThrArgValLysGlyTyrPheLeuLeuAspAsnTyrTleProThrPheValCysSerVal 40
 DB 196 ACTAGAGTAAAGGATGTTCTTCTCGACAAATTATATACCCACATTTATCTGCTCTGTC 255
 QY 41 11eTyrLeuLeuValTyrPheLeuGlyProLysTyrMetLysAsnArgGlnProPheSer 60
 DB 256 ATATATTTTAC:TAATTGTATGCTGGACCAAAATACATGAGGAATAAACACCCATCTCT 315
 QY 61 CysArgGlyIleLeuGlnLeuTyrAsnTyrLeuGlyLeuThrLeuLeuSerLeuTyrMetPhe 80
 DB 316 TCGGGGGGCAATTTAGTGTGTATTAACCTTGGATCATCATCTGCTCTCTGTATATGTTTC 375
 QY 81 TyrGluLeuValIleGlyValIlePheGlyLysTyrAsnPhePheCysGlnGlyThrArg 100
 DB 376 TGTGATTTAGTAAACAGAGATATGAGAGAGGCAATATCTTCTGTAGGGCAGCAGC 435
 QY 101 SerAlaGlyGluSerAspMetLysIleIleArgValLeuIleTyrPheTyrPheSerLys 120
 DB 436 ACCGGCAGGAGAAATCAGATATCAAGATTAACGGTGTCTGCTGCTGCTACTTCTCTCCAAA 495
 QY 121 LeuIleGluPheMetAspThrPhePhePheIleLeuArgLysAsnAsnHisGlnIleThr 140
 DB 496 CTATAGAAATTTATGACACACTTCTTCTCTCATCTTCTGCGCAAGAACACACACATCAG 555
 QY 141 ValLeuHisValTyrHisAlaThrMetLeuAsnIleTyrPheValMetAsnTyrP 160
 DB 556 GTCTGTGACGTGTACACACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 615
 QY 161 ValProCysGlyHisSerTyrPheGlyAlaThrLeuAsnSerPheIleHisValLeuMet 180
 DB 616 GTCCCTCTGGGGCAGCTTATTTTGGTCCACACTTAATAGCTTCATCCACGCTCTCATG 675
 QY 181 TyrSerTyrTyrGlyLeuSerSerIleProSerMetArgProTyrLeuTyrTrpLysLys 200
 DB 676 TACTCTTACTATGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 735
 QY 201 TyrIleThrGlnGlyGlnLeuValGlnPheValIleThrIleGlnThrThrCysGly 220
 DB 736 TACATCACTCAGGGGCACTGCTTCACTTGTATGAGTATGAGTATGAGTATGAGTATGAG 795
 QY 221 ValPheTyrProCysSerPheProLeuGlyTyrPhePheGlnIleGlyTyrMetIle 240
 DB 796 GTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 855
 QY 241 SerLeuIleAlaLeuPheThrAsnPheTyrIleGlnThrTyrAsnLysLysGlyAlaSer 260
 DB 856 TCCCTCATGCTCTCTTCCAAACCTTCTACATCAGACCTACACAAACAAAGAGGGGCTCC 915
 QY 261 ArgArgLysAspHisLeuLysGlyHisGlnAsnGlySerValAlaIaValAsnGlyHis 280
 DB 916 CGAAGGAAAGACACCTCAAGAGACACACAGAAATGAGTCTGCTGCTGCTGCTGCTGCTG 975
 QY 281 ThrAsnSerPheProSerSerLeuAsnSerValLysTyrArgLysGlnArgLysAsp 299
 DB 976 ACCCAACAGTTTTCATCTCTGAGAAACCAATGAGAAACCAACCAACCAACCAACCAAT 1032
 RESULT 10
 AAS44919
 ID AAS44919 standard; DNA; 3083 BP.
 XX
 XX AC AAS44915;
 XX XX
 XX DT 18-DEC-2001 (first entry)

Alignment Scores:
 Pred. No.: 3,180-160 Length: 2769
 Score: 1559.00 Matches: 278
 Percent Similarity: 97.34% Conservative: 13

Human contig polynucleotide sequence #172.

Mammal; human; rhesus monkey; baker's yeast; fission yeast; Norway rat; mouse; Chinese hamster; African clawed frog; fruit fly; dog; leukaemia; cancer; lymphoma; neuroblastoma; autoimmune disorder; cell proliferation; nervous system disorder; inflammatory disorder; cell differentiation; ds; angiogenesis; stem cell growth factor; activin; inhibin; cartilage; burn; genetic disorder; bone regeneration; tendon; ligament; tissue repair; cystic; antirheumatic; antiarthritic; vulnary; antiinflammatory; antibacterial; immunosuppressive; vasotropic; antiparkinsonian; neuroprotective; osteopathic; antidiabetic; antialthmatic; antiallergic; immunostimulant; analgesic; gene therapy.

OS Homo sapiens.
XX Synthetic.
XX
XX W0200164834-A2.
XX
XX 07-SEP-2001.
XX
XX 26-FEB-2001; 2001W0-0S04926.
XX
XX 28-FEB-2000; 2000US-0515136.
XX
XX 18-MAY-2000; 2000US-0577409.
XX
XX 17-JUN-2000; 2000US-0597707.
XX
XX 14-JUL-2000; 2000US-0616807.
XX
XX 19-SEP-2000; 2000US-0664641.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YF, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
XX Xue AJ, Yang Y, Wehrman T, Wang J, Ma Y, Wang D, Chen R, Xu C;
XX Dmanac P;
XX
XX WPI; 2001-589862/66.
XX
XX P-PSDB; AAU28019.
XX
XX Novel polypeptides and nucleic acids obtained from cDNA libraries
XX prepared from various human tissues, for diagnosis, treatment of
XX cancer, neurological, inflammatory disorders and for use in arrays for
XX detection
XX
XX Claim 1; SEQ ID NO 516; 153pp; English.
XX
XX Sequences AA54576-AA544919 represent full-length polynucleotides and
XX contig polynucleotides encoding polypeptides of the invention. The DNA
XX and protein sequences are useful for the treatment, diagnosis and
XX prevention of various types of disorder in a mammalian subject such as a
XX human, dog, monkey, mouse, hamster or rat. The disorders include cancers
XX such as leukaemia, lymphoma and neuroblastoma, autoimmune disorders such
XX as multiple sclerosis, connective tissue disease, rheumatoid arthritis,
XX diabetes mellitus, allergic rhinitis, asthma and eczema, nervous system
XX disorders such as Parkinson's disease, Alzheimer's disease, Huntington's
XX chorea, amyotrophic lateral sclerosis, spinal muscular atrophy and
XX Wernicke disease, inflammatory disorders such as nephritis, Crohn's
XX disease, ischaemia reperfusion injury, shock, sepsis and inflammatory
XX bowel disease. The sequences exhibit activity relating to angiogenesis,
XX cell proliferation, cell differentiation, stem cell growth factor,
XX activin or inhibin, therefore, they can be used to manipulate stem cells
XX in culture to give rise to neuroepithelial cells that can be used to
XX augment or replace cells damaged by illness, accidental damage or genetic
XX disorders. The sequences may also be used for regeneration of bone,
XX cartilage, tendons and ligaments and in tissue repair and burn healing.
XX Note: Some sequences for this patent did not form part of the printed
XX specification, but were obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pat_sequences.
XX
XX Sequence 3083 BP; 884 A; 594 C; 607 G; 996 T; 2 other;
XX
XX Alignment Scores:
XX Pred. No.: 3,7c 160 Length: 3083
XX Score: 1559.00 Matches: 278

Percent Similarity: 97.32% Conservat: 14
Best Local Similarity: 92.98% Mismatches: 8
Query Match: 94.43% Indels: 0
DB: 22 Gaps: 0
US-09-624-670-64 (1-299) X AA544919 (1-3083)
QY 1 MetGluHisPheAspAlaSerLeuSerThrTyrPheLysAlaPheLeuGlyProArgasp 20
DB 136 ATGAAATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 195
QY 21 ThrArgValLysGlyTrpPheLeuLeuAspAsnTyrLeuPheThrPheValCysSerVal 40
DB 196 ACTAGACTAAAGGACATGCTTCTCTGCGACAAATATATATATATATATATATATAT 255
QY 41 IleTyrLeuLeuLeuValTrpLeuGlyProLysTyrMetLysAsuArgGlnProPheSer 60
DB 256 ATATATTTACTAAATGATGCTGCGACAAATATATGACAAATATATGACAAATAT 315
QY 61 CysArgGlyIleLeuGlnLeuTyrAsnLeuGlyLeuIleLeuLeuSerLeuTyrMetPhe 80
DB 316 TGGAGAGGATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 375
QY 81 TyrGluLeuValThrGlyValTrpGluGlyLysTyrAsnPhePheCysGlnGlyThrArg 100
DB 376 TGTGAGTTAGTAACAGCAGTATGCGAAGCAAAATATAATTTCTCTCTCTCTCTCTCT 435
QY 101 SerAlaGlyGluSerAspMetLysIleLeuValLeuIleTyrTyrTyrPheSerLys 120
DB 436 ACCGACGAGATACATATGAGATATATGAGATATATGAGATATATGAGATATATG 495
QY 121 LeuIleGluPheMetAspThrPhePhePheIleLeuArgLysAsuHisGlnIleThr 140
DB 496 CTCATAGAAATTTATGACAAATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 555
QY 141 ValLeuHisValTyrHisHisAlaThrMetLeuAsnIleTyrPheValMetAsnTrp 160
DB 556 GTCTTCACGCTTACCAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 615
QY 161 ValProCysGlyHisSerTyrPheGlyAlaThrLeuAsuSerPheIleHisValLeuMet 180
DB 616 GTCCCTCGCGCCACTCTTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 675
QY 181 TyrSerTyrGlyLeuSerSerIleProSerMetArgProTyrLeuSerPheLys 200
DB 676 TACTCTTACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 735
QY 201 TyrIleThrGlyGlnLeuValGlnPheValLeuIleIleIleIleIleIleIleIle 220
DB 736 TACATGACACAGGGGAGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 795
QY 221 ValPheTrpProCysSerPheProLeuGlyTrpLeuPhePheGlnIleIleTyrMetIle 240
DB 796 GTCACTGCGCCGCTGACATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 855
QY 241 SerLeuIleAlaLeuPheThrAsnIleTyrIleGlnIleTyrAsnLysLysGlyValSer 260
DB 856 TCCTGATTTGCT 915
QY 261 ArgArgLysAspHisLeuLysGlyHisGlnAsnLysSerValAlaIleValAsnGlyHis 280
DB 916 GTAAAGAAAGAAATATTAAGAGACACAGAGATGCTGCTGCTGCTGCTGCTGCTG 975
QY 281 ThrAsnSerPheProSerLeuGluAsnSerValLysProArgLysGlnArgLysAsp 299
DB 976 ACCCAACAGCTTTTACCGCTGCAAAACAAATGCGAAGCAAAACAGCTGCTGCTG 1042
RESULT 11
ABK46367
ID ABK46367 standard; cDNA; 914 BP.
XX
XX ABK46367;
AC
XX

DT 05-JUN-2002 (first entry)
 XX Human elongase HSELO1 cDNA.
 KW ss: gene; elongase; polyunsaturated fatty acid; pufo; transgenic plant;
 KW transgenic non-human animal; plant oil; arachidonic acid; nutritional;
 KW pharmaceutical; cosmetic; animal feed; restenosis; angioplasty; AIDS;
 KW acquired immunodeficiency syndrome; multiple sclerosis; cachexia; asthma;
 KW inflammatory skin disease; osteoporosis; kidney stones; cancer; eczema;
 KW inflammation; rheumatoid arthritis; psoriasis; placental aggregation;
 KW vasodilation; cholesterol reduction; gastrointestinal bleeding.
 XX Homo sapiens.
 OS
 PN WO200208401-A2.
 XX
 PD 31-JAN-2002.
 XX
 PF 24-JUL-2001; 2001WO US3259.
 XX
 PR 24-JUL-2000; 2000US-0624579.
 PR 11-JUL-2001; 2001US-0903456.
 XX
 PA (ABBO) ABBOTT LAB.
 XX
 PI Mukerji P, Das T, Huang Y, Parker-Barnes JM, Leonard AE;
 PI Thurmond J, Pereira SL;
 XX
 DR WPI; 2002-172011/22.
 DR P-PSDB: AAU87830.
 XX
 PT Isolated nucleic acid sequences encoding elongase proteins, useful in
 PT the production of polyunsaturated fatty acids, e.g. arachidonic acid,
 PT which can then be used nutritional compositions and pharmaceutical
 PT compositions (for treating AIDS) -
 XX
 PS Example 16; Fig 43; 27pp; English.
 XX
 CC The invention relates to isolated nucleic acid sequences encoding
 CC elongase proteins and the elongase proteins themselves. Also
 CC included are a purified polypeptide which elongates polyunsaturated
 CC fatty acids and has at least 30% amino acid similarity to the amino acid
 CC sequence to an elongase protein, a vector comprising the nucleic
 CC acid, a plant cell (or tissue or whole plant) comprising the vector and
 CC expressing the nucleic acid, a plant oil or acid expressed by the
 CC transgenic plant and a transgenic non-human animal expressing elongase
 CC in its fluid. The nucleic acids and elongase proteins may be used
 CC directly or indirectly in the production of polyunsaturated fatty acids
 CC (puta) for a arachidonic acid, which can then be used nutritional
 CC compositions, pharmaceutical compositions, cosmetics and animal feeds.
 CC The pharmaceutical compositions may be used in the treatment of
 CC restenosis after angioplasty, AIDS (acquired immunodeficiency syndrome),
 CC multiple sclerosis, inflammatory skin diseases, osteoporosis, kidney or
 CC urinary tract stones, malignant cancer, cachexia associated with cancer,
 CC eczema, symptoms of inflammation, rheumatoid arthritis, asthma and
 CC psoriasis. They are also useful for inhibiting platelet aggregation,
 CC inducing vasodilation, reducing cholesterol, reducing or preventing
 CC gastrointestinal bleeding and side effects of non-steroidal
 CC anti-inflammatory drugs. The present sequence encodes an elongase
 CC of the invention.
 XX
 XX Sequence 914 BP; 236 A, 223 G, 199 G, 256 T, 0 other.

Alignment Scores:
 Pcd. No.: 8,61e-161 Length: 914
 Score: 1558.00 Matches: 278
 Percent Similarity: 97.32% Conservatives: 13
 Best Local Similarity: 92.98% Mismatches: 8
 Query Match: 94.37% Indels: 0
 DB: 24 Gaps: 0

US-09-624-670-64 (1-299) x ABK46367 (1-914)

Breast cancer; diagnosis; prognosis; detection; screening;
 antibody; oestrogen receptor; anti-oestrogen; immune response;
 lymph node; metastases; tumour; BCR3; BCQ8; BCQ5; BCR1; BCW2;

QY 1 MetGluHisPheAspAlaSerLeuSerThrTyrPheLysAlaPheLeuGlyProArgAsp 20
 DB 1 ATCCAAACATTTTCATGCATCACTTAGCTACCTATTTCAAGGCATTCCTAGGCGCTCGAGAT 60
 QY 21 ThrArgValLysGlyTrpPheLeuLeuAspAsnTyrIleProThrPheValCysSerVal 40
 DB 61 ACTAGAGTAAGAGTGGTTCTCTCTGGCAATATATACCCACATTTATCTGTCTCTGTC 120
 QY 41 IleTyrLeuLeuIleValTrpLeuGlyProLysTyrMetLysAsnArgGlnProPheSer 60
 DB 121 ATATATTTACTAATTCATGGCTGGCACCACCAATATACATGAGCAATAAACAGCCATCTCT 180
 QY 61 CysArgGlyIleLeuGlnLeuTyrAsnLeuGlyLeuThrLeuLeuSerLeuTyrMetPhe 80
 DB 181 TGC CGGGGATTTAGTGGTGATATAACCTTGGACTCACACTGCTCTCTGTATATGTTTC 240
 QY 81 TyrGluLeuValThrGlyValTDPGluGlyLysTyrAsnPhePheCysGlnGlyThrArg 100
 DB 241 TGTGGTTAGTACAGGAGTATGGGAAGCAATACAACTTCTCTGTGAGGCACACGC 300
 QY 101 SerAlaGlyGluSerAspMetLysIleIleArgValLeuTyrTrpTyrPheSerLys 120
 DB 301 ACCGAGGAGATCAGATATGAAGATATCCGTTCTCTCTGGTGTACTACTTCCAAA 360
 QY 121 LeuIleGluPheMetAspThrPhePheIleLeuArgLysAsnAsnHisGlnIleThr 140
 DB 361 CTCATAGAAATTAATGGACACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
 QY 141 ValLeuHisValTyrHisHisAlaThrMetLeuAsnIleTrpTrpPheValMetAsnTrp 160
 DB 421 GTCTGTGACGCTATACCACTGCTGATGCTGAACATCTGGTGGTTTGTGATGAAGTGG 480
 QY 161 ValProCysGlyHisSerTyrPheGlyAlaThrLeuAsnSerPheIleHisValLeuMet 180
 DB 481 GTCCCTCTGGGCCACTCTTATTTGTGTGCCACACTTAATAGCTTCATCCACGTCCTCATG 540
 QY 181 TyrSerTyrTyrGlyLeuSerSerIleProSerMetArgProTyrLeuTrpTrpLys 200
 DB 541 TACTCTTACTATGCTTTTGTCTGCTACCTCCCTTCCATCCCTGCTCCATCCCTGCTGGAAGAAG 600
 QY 201 TyrIleThrGlnGlyGlnLeuValGlnPheValLeuThrIleIleGlnThrCysGly 220
 DB 601 TACATCAATCAAGAGTAAATTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 660
 QY 221 ValPheTrpProCysSerPhePheProLeuGlyTrpLeuPhePheGlnIleGlyTyrMetIle 240
 DB 661 GTCATCTGGCGCTGCACATTCCT 720
 QY 241 SerLeuIleAlaLeuPheThrAsnPheTyrIleGlnThrTyrAsnLysLysGlyAlaSer 260
 DB 721 TCCCTGATGCT 780
 QY 261 ArgArgLysAspHisLeuLysGlyHisGlnAsnGlySerValAlaAlaValAsnGlyHis 280
 DB 781 CGAG 840
 QY 281 ThrAsnSerPheProSerLeuGluAsnSerValLysProArgLysGlnArgLysAsp 299
 DB 841 ACCAAGACATTTTCCACCTTCCACCTTCCACCTTCCACCTTCCACCTTCCACCTTCCACCTTCC 897

RESULT 12
 AAA54132
 ID AAA54132 standard; DNA; 2710 BP.
 XX
 AC AAA54132;
 XX
 DT 08-FEB-2001 (first entry)
 XX
 DE Breast cancer protein BCR2 coding sequence.
 XX
 KW Breast cancer; diagnosis; prognosis; detection; screening;
 KW antibody; oestrogen receptor; anti-oestrogen; immune response;
 KW lymph node; metastases; tumour; BCR3; BCQ8; BCQ5; BCR1; BCW2;

PA (UYJO) JOHN HOPKINS UNIVERSITY.
 XX Ishizaka K, Martens CL, Moore KW;
 XX WPI; 1988-280165/40.
 DR P-PSDB; AAP82590.
 XX Nucleic acid encoding glycosylation inhibiting peptide - capable of
 PT suppressing IgE immunoglobulin responses, for use as antiinflammatory
 PT agents.
 XX Claim 1; Page 16-21, 29pp, English.
 PS The sequence encodes a polypeptide with G1F activity, which has the
 XX following biological activities: IgE binding factor switching activity,
 CC inhibition of IgE-induced Fe epsilon receptor expression, and inhibition
 CC of phospholipase A2 activity after dephosphorylation.
 XX Sequence 2571 BP; 681 A; 573 C; 540 G; 777 T; 0 other:
 SQ
 Alignment Scores:
 Pred. No.: 1-16e-152 Length: 2571
 Score: 1489.50 Matches: 283
 Percent Similarity: 96.94% Conservative: 1
 Best Local Similarity: 96.59% Mismatches: 2
 Query Match: 90.22% Indels: 9
 DB: 9 Gaps: 1
 US-09-624-670-64 (1-2571) x RAN01168 (1-2571)
 QY 7 SerLeuSerThrTyrPhoLeuGlyAlaPheLeuGlyProArgAspThrArgValGlyTyr 26
 Db 3 TCACCTCAGTACGATTATTTAAAGCC-TTCGTGAGCGCGGAGATACAGAGTCAAGAGATGG 61
 QY 27 PheLeuLeuAspAsnTyrIleProThrPheValCysSerValIleTyrLeuLeuIleVal 46
 Db 62 TTCTCTCCGCGCAATATACATCCCTACGTTGTCTGTCTCTCTTATTACTTACTTACTTGT 121
 QY 47 TrpLeuGlyProLysTyrMetLysAsnArgGlnProPheSerCysArgGlyIleLeuGln 65
 Db 122 TGGTGGGACGAAATAATATAAAGAAAGAGAGATGTTCTTGGAGAGC-ATCATGTGAG 180
 QY 67 LeuTyrAsnLeuGlyIleThrLeuLeuSerLeuTyrMetPheTyrGluLeuValThrGly 86
 Db 181 TTGTATATTTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 240
 QY 87 ValTrpGluGlyLysTyrAsnPhePheCysGlnGlyThrArgSerAlaGlyGluSerAsp 106
 Db 241 GTCTGGGAGGCAATATACACTTTTCTGCGAGGCAACAGCAACGCGGAGAAATCCGAT 300
 QY 107 MetLysIleLeuAcqValLeuTrpTyrTyrPheSerLysLeuIleGluPheMetAsp 126
 Db 301 ATAAAGATATAGAGATATATAGAGATATATAGAGATATATAGAGATATATAGAGATAT 360
 QY 127 ThrPhePhePheIleLeuArgLysAsnAsnHisGlnIleThrValLeuHisValTyrHis 146
 Db 361 ATGTTTCTTTTAT 420
 QY 147 HisAlaThrMetLeuAsnIleTyrTrpPheValMetAsuTrpValProGlyHisSer 166
 Db 421 CACCTACCATCTCTCAACATC.....GTTCCTCTCGGCCCATTC 459
 QY 167 TyrPheGlyAlaThrLeuAsnSerPheIleHisValLeuMetTyrSerTyrTyrGlyLeu 186
 Db 460 TATTTGATGAGAAATATAAATATATATATATATATATATATATATATATATATATAT 519
 QY 187 SerSerIleProSerMetArgTyrIleLeuTrpTrpLysTyrIleThrGlnGlyGln 206
 Db 520 TCTTCTATCTGAT 579
 QY 207 LeuValGlnPheValLeuThrIleIleGlnThrThrCysGlyValPheTrpProCysSer 226
 Db 580 GTGGGAGAGTGGTAT 639
 QY 227 PheProLeuGlyTyrTrpLeuPhePheClnIleGlyTyrMetIleSerLeuIleAlaLeuPhe 246
 Db 640 TTCCTCTCGGAGTGGTAT 699
 QY 247 ThrAsnPheTyrIleGlnThrTyrAsnLysLysGlyAlaSerArgArgLysAspHisLeu 266
 Db 700 ACAAACTTCTAT 759
 QY 267 LysGlyHisGlnAsnGlySerValAlaAlaValAsnGlyHisThrAsnSerPheProSer 286
 Db 760 AAGAGGACACAAAGAGGAGTCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 819
 QY 287 LeuGluAsnSerValLysProArgLysGlnArgLysAsp 299
 Db R20 CTGTAAGAAAGAGTAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 358
 RESULT 14
 ABL90374
 ID ABL90374 standard; cDNA; 1997 BP.
 XX
 AC ABL90374;
 XX
 DT 24-MAY-2002 (first entry)
 XX
 DE Human polynucleotide SEQ ID NO 936.
 KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
 KW antiallergic; hepatocytropic; antidiabetic; antinflammatory; antileuc;
 KW vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;
 KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; human; secreted protein; gene; ss.
 OS Homo sapiens.
 PN WO200190304-A2.
 PD 29-NOV-2001.
 XX
 PF 18-MAY-2001; 2001WO-US16450
 PR 19-MAY-2000, 2000US-205515P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Birse CE, Rosen CA
 XX
 DR WPI; 2002-132018/16.
 DR P-PSDB; ABB89965.
 XX
 PT Novel 1405 isolated polypeptides, useful for diagnosis, treatment and
 PT prevention of neural, immune system, muscular, reproductive,
 PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative
 PT disorders -
 PS
 PS Claim 4; SEQ ID NO 936; 2081pp + Sequence listing; English.
 CC The invention relates to novel genes (ABL89449-ABL90853) and proteins
 CC (AAB89440-AB899444) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (auto)antibodies are useful
 CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
 CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
 CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital,
 CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemia;
 CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 CC and parasitic infections.
 CC Note: The sequence data for this patent did not form part of the

CC printed specification, but was obtained in electronic format directly
 from WFO at <http://wfo.int/4/pub/aligned/seq/sequences>.

XX Sequence 1997 HP: 483 A; 487 C; 460 G; 553 T; 14 other;

Alignment Scores:

Pred. No.: 8,82e 147 Length: 1947
 Score: 1344.00 Matches: 247
 Percent Similarity: 98.41% Conservative: 11
 Best Local Similarity: 94.05% Mismatches: 4
 Query Match: 81.44% Indels: 0
 DB: 24 Gaps: 0

US 09 624-670-64 (1-299) x ABL40474 (1-1997)

QY 1 MetGluHisPheAspAlaSerLeuSerThrTyrPheValAlaPheLeuGlyProArgAsp 20
 DB 106 ATGAGAACATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 165
 QY 21 ThrArgValLysGlyTyrPheLeuLeuAspAsnTyrIleProThrPheValCysSerVal 40
 DB 166 ACTAGAGTAAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 225
 QY 41 IleTyrLeuLeuIleValTyrLeuGlyProLysTyrMetLysAsnArgGlnProPheSer 60
 DB 226 ATATATTACTATTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 285
 QY 61 CysArgGlyTyrLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
 DB 286 TGCGGGGGGATTTAGTGGGGTATATGCTTGGATGATGATGATGATGATGATGATGAT 345
 QY 81 TyrGluLeuValThrGlyValTyrGlyLysTyrAsnGlnPheCysGlnGlnGlyThrArg 100
 DB 346 TGTGAGTACTAAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 405
 QY 101 SerAlaGlyGlnSerAspMetLysIleIleArgValLeuTyrTrpTyrThrPheSerLys 120
 DB 406 ACCGACAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 465
 QY 121 LeuIleGluPheMetAspThrPhePheIleLeuArgLysAsnHisGlnIleThr 140
 DB 466 CTATACAAATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 525
 QY 141 ValLeuIleValTyrHisHisAlaThrMetLeuAsnIleTyrTrpPheValMetAsnTrp 160
 DB 526 GTCCTGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 585
 QY 161 ValProCysGlyHisSerTyrPheGlyAlaThrLeuAsnSerPheIleIleHisValLeuMet 180
 DB 586 GTCCCTCGAGACATCTATTATTTGGAGGACATTTAATAGGTTTATGATGATGATG 645
 QY 181 TyrSerTyrTyrGlyLeuSerGlnIleProSerMetArgGlyTyrLeuGlyTyrPheLys 200
 DB 646 TACTTACTATGTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 705
 QY 201 TyrIleThrIleGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 220
 DB 706 TATATCACTCAGGGGAGTGGCTTCAGTGTGGATGATGATGATGATGATGATGATGATG 765
 QY 221 ValPheTyrPheCysSerPhePheLeuGlyTyrLeuPhePheIleIleTyrMetIle 240
 DB 766 GTATCTGGGGTGCATATTCCTCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 825
 QY 241 SerLeuLeuValGlnPheAspPhePheValThr 260
 DB 826 TCCGTGATGCTCTCTTCATCAAAAGCTTCTCATATTCAG 861

RESULT 15

AA007290

10 AA007290 standard: cDNA; 97% HP.

XX

Ac

XX

DT 10 AUG 2001 (first entry)
 XX Human cold-induced glycoprotein 40-like protein (hclq40L) cDNA.
 XX Human: cold-induced glycoprotein 40 like protein; hclq40L; anorectic;
 KW drug screening; gene therapy; restriction fragment length polymorphism;
 KW RFLP; chromosomal mapping; tissue typing; toxicosis; metabolic disorder;
 KW obesity-related disorder; aberrant food intake; energy expenditure;
 KW glucose metabolism; fat metabolism; type II diabetes mellitus; NIDDM;
 KW hypertension; coronary heart disease; hypercholesterolaemia; gallstones;
 KW osteoarthritis; cancer; sleep apnea; ss.
 XX Homo sapiens.
 XX OS
 XX Key Location/Qualifiers
 FH CDS 1..975
 FT /ftaq-4
 FT /product: "Human cold induced glycoprotein 40 like
 FT protein (hclq40L)."
 XX W020011013-A1.
 XX 03 MAY 2001.
 XX 27-OCT-2000: 2000W0-3529559.
 XX 28 OCT-1999: 99US 0161978.
 XX 29 OCT 2000: 2000US-333444.
 XX (CURA) CURAGEN CORP.
 XX Lewin DA, Stewart TA;
 XX WPI: 2001 328652/44.
 XX P-PSDB: AAE02842.
 XX Human cold-induced glycoprotein-like-40 protein and nucleic acids
 encoding the protein useful for treating obesity related disorders,
 e.g. metabolic disorders, aberrant food intake, energy expenditure or
 fat metabolism.
 XX Claim 8; Fig 2A; 97pp; English.

The present sequence is human cold induced glycoprotein 40 like protein
 (hclq40L) cDNA. The hclq40L proteins are useful as immunogens to raise
 anti-hclq40L antibodies, to screen drugs or compounds that modulate
 protein activity or expression and to treat disorders characterised by
 insufficient or excessive production of an hclq40L protein or production
 of hclq40L protein forms that have decreased or aberrant activity
 compared to wild-type protein. The nucleic acids are also used to
 express hclq40L protein for gene therapy applications, to detect hclq40L
 mRNA in a biological sample or a genetic lesion in hclq40L and as
 additional DNA markers for restriction fragment length polymorphisms
 (RFLP). The hclq40L is used in screening assays, in detection assays
 such as chromosomal mapping, cell and tissue typing, forensic and
 biotay and in preventive medicine (e.g. diagnostic or prognostic
 assays, monitoring clinical trials, and pharmacogenomics). The hclq40L is
 used to treat obesity-related disorders (e.g. metabolic disorders),
 aberrant food intake, energy expenditure, glucose metabolism, fat
 metabolism, type II diabetes mellitus (NIDDM), hypertension, coronary
 heart disease, hypercholesterolaemia, gallstones, osteoarthritis and
 cancers of reproductive organs or sleep apnea.

XX SEQIDNO: 975 HP: 244 A; 246 C; 228 G; 257 T; 6 other;

Alignment Scores:

Pred. No.: 7,09e 116 Length: 975
 Score: 1148.30 Matches: 204
 Percent Similarity: 97.71% Conservative: 10
 Best Local Similarity: 93.12% Mismatches: 6
 Query Match: 69.54% Indels: 0
 DB: 22 Gaps: 0

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 15, 2003, 21:38:16 : Search time 54.63% Seconds
(without alignments)
1678.203 Million cell updates/sec

Title: US-09-624-670-64

Period score: 1651

Sequence: 1 MEHFDASLTYKFAFLGRD. HTNSFSPLENSVPRKQRKD 299

Scoring table:

BLASTSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-O=/cgn2_1/USPVO-Spool/US09624670/runat_11062003_075431_11654/app_query.fasta_1.910
-DB=Issued_Patents_NA -QMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=6 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USRR=US09624670 -CGN_1_84=runat_11062003_075431_11654 -NCPU=6 -ICPU=3
-NO_MMAP -LARGQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOB=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA.*

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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PGTUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Prod No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	476.5	28.9	1482	4	US-09-149-476-258
2	476.5	28.9	1542	4	US-09-149-476-259
3	326.5	19.8	1854	1	US-08-249-420-1
4	326.5	19.8	1854	2	US-08-249-420-1
5	255	15.4	590	4	US-08-737-663-1
6	249	15.1	934	4	US-09-145-828A-10
7	219	13.3	989	1	US-07-885-970A-7
8	219	13.3	989	1	US-08-298-687A-7
9	219	13.3	989	1	US-08-530-797-6
10	219	13.3	989	1	US-08-298-829-7
11	219	13.3	989	2	US-08-787-335-6
12	209	12.7	587	4	US-09-145-828A-9

13	189	11.4	124	4	US-09-172-108-45	Sequence 45, Appl
14	138.5	8.4	834	4	US-09-149-476-259	Sequence 259, Appl
15	100.5	6.1	22846	2	US-08-469-461-3	Sequence 3, Appl
16	100.5	6.1	22846	3	US-07-890-609-3	Sequence 3, Appl
17	99	6.0	4079	1	US-08-121-057-2	Sequence 2, Appl
18	99	6.0	4079	2	US-08-509-187D-2	Sequence 2, Appl
19	99	6.0	4079	3	US-09-131-396-2	Sequence 2, Appl
20	99	6.0	4079	5	PCT-US93/09704A-2	Sequence 2, Appl
21	98	5.9	6002	4	US-09-345-882-3	Sequence 4, Appl
22	97.5	5.9	4011	1	US-08-131-057-3	Sequence 3, Appl
23	97.5	5.9	4011	2	US-08-509-187D-3	Sequence 3, Appl
24	97.5	5.9	4011	3	US-08-121-396-3	Sequence 3, Appl
25	97.5	5.9	4011	5	PCT-US93/09704A-3	Sequence 3, Appl
26	95	5.8	2274	3	US-08-452-459-13	Sequence 13, Appl
27	95	5.8	2274	4	US-08-452-459-13	Sequence 13, Appl
28	95	5.8	2274	3	US-08-452-459-13	Sequence 13, Appl
29	95	5.8	2274	4	US-08-716-873-27	Sequence 27, Appl
30	95	5.8	2274	4	US-09-368-431-27	Sequence 27, Appl
31	95	5.8	2274	4	US-09-414-006-21	Sequence 13, Appl
32	93.5	5.6	2274	4	US-09-414-006-21	Sequence 13, Appl
33	93.5	5.6	90050	4	US-09-447-223-13	Sequence 5, Appl
34	93	5.6	1553	3	US-08-245-041-5	Sequence 21, Appl
35	93	5.6	1553	3	US-08-452-459-21	Sequence 21, Appl
36	93	5.6	1553	4	US-08-423-752-21	Sequence 21, Appl
37	93	5.6	1553	4	US-08-716-873-35	Sequence 35, Appl
38	93	5.6	1553	4	US-09-368-431-35	Sequence 35, Appl
39	92.5	5.6	1553	4	US-09-414-006-21	Sequence 21, Appl
40	91.5	5.5	1714	3	US-09-447-223-21	Sequence 111, Appl
41	91.5	5.5	8789	1	US-08-961-083-3	Sequence 3, Appl
42	91.5	5.5	15213	4	US-08-328-254-5	Sequence 5, Appl
43	91.5	5.5	15213	4	US-08-961-527-26	Sequence 26, Appl
44	89.5	5.4	1277	4	US-08-790-912-1	Sequence 1, Appl
45	89.5	5.4	2383	4	US-09-347-803-3	Sequence 3, Appl
					US-09-221-017B-629	Sequence 629, Appl

ALIGNMENTS

RESULT 1

US-09-149-476-258
; Sequence 258, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P200291
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
; EARLIER FILING DATE: 1997-05-23

1 EARLIER APPLICATION NUMBER: 60/047,584
2 EARLIER FILING DATE: 1997-05-23
3 EARLIER APPLICATION NUMBER: 60/047,617
4 EARLIER FILING DATE: 1997-05-23
5 EARLIER APPLICATION NUMBER: 60/047,618
6 EARLIER FILING DATE: 1997-05-23
7 EARLIER APPLICATION NUMBER: 60/047,504
8 EARLIER FILING DATE: 1997-05-23
9 EARLIER APPLICATION NUMBER: 60/047,592
10 EARLIER FILING DATE: 1997-05-23
11 EARLIER APPLICATION NUMBER: 60/047,581
12 EARLIER FILING DATE: 1997-05-23
13 EARLIER APPLICATION NUMBER: 60/047,584
14 EARLIER FILING DATE: 1997-05-23
15 EARLIER APPLICATION NUMBER: 60/047,500
16 EARLIER FILING DATE: 1997-05-23
17 EARLIER APPLICATION NUMBER: 60/047,587
18 EARLIER FILING DATE: 1997-05-23
19 EARLIER APPLICATION NUMBER: 60/047,492
20 EARLIER FILING DATE: 1997-05-23
21 EARLIER APPLICATION NUMBER: 60/047,598
22 EARLIER FILING DATE: 1997-05-23
23 EARLIER APPLICATION NUMBER: 60/047,613
24 EARLIER FILING DATE: 1997-05-23
25 EARLIER APPLICATION NUMBER: 60/047,582
26 EARLIER FILING DATE: 1997-05-23
27 EARLIER APPLICATION NUMBER: 60/047,596
28 EARLIER FILING DATE: 1997-05-23
29 EARLIER APPLICATION NUMBER: 60/047,612
30 EARLIER FILING DATE: 1997-05-23
31 EARLIER APPLICATION NUMBER: 60/047,632
32 EARLIER FILING DATE: 1997-05-23
33 EARLIER APPLICATION NUMBER: 60/047,601
34 EARLIER FILING DATE: 1997-05-23
35 EARLIER APPLICATION NUMBER: 60/043,580
36 EARLIER FILING DATE: 1997-04-11
37 EARLIER APPLICATION NUMBER: 60/043,568
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39 EARLIER APPLICATION NUMBER: 60/043,314
40 EARLIER FILING DATE: 1997-04-11
41 EARLIER APPLICATION NUMBER: 60/043,569
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43 EARLIER APPLICATION NUMBER: 60/043,311
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48 EARLIER FILING DATE: 1997-04-11
49 EARLIER APPLICATION NUMBER: 60/043,669
50 EARLIER FILING DATE: 1997-04-11
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53 EARLIER APPLICATION NUMBER: 60/043,313
54 EARLIER FILING DATE: 1997-04-11
55 EARLIER APPLICATION NUMBER: 60/043,672
56 EARLIER FILING DATE: 1997-04-11
57 EARLIER APPLICATION NUMBER: 60/043,315
58 EARLIER FILING DATE: 1997-04-11
59 EARLIER APPLICATION NUMBER: 60/048,974
60 EARLIER FILING DATE: 1997-06-06
61 EARLIER APPLICATION NUMBER: 60/056,886
62 EARLIER FILING DATE: 1997-08-22
63 EARLIER APPLICATION NUMBER: 60/056,877
64 EARLIER FILING DATE: 1997-08-22
65 EARLIER APPLICATION NUMBER: 60/056,889
66 EARLIER FILING DATE: 1997-08-22
67 EARLIER APPLICATION NUMBER: 60/056,894
68 EARLIER FILING DATE: 1997-08-22
69 EARLIER APPLICATION NUMBER: 60/056,630
70 EARLIER FILING DATE: 1997-08-22
71 EARLIER APPLICATION NUMBER: 60/056,878
72 EARLIER FILING DATE: 1997-08-22
73 EARLIER APPLICATION NUMBER: 60/056,909
74 EARLIER FILING DATE: 1997-08-22
75 EARLIER APPLICATION NUMBER: 60/056,662
76 EARLIER FILING DATE: 1997-08-22
77 EARLIER APPLICATION NUMBER: 60/056,872
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81 EARLIER APPLICATION NUMBER: 60/056,664
82 EARLIER FILING DATE: 1997-08-22
83 EARLIER APPLICATION NUMBER: 60/056,876
84 EARLIER FILING DATE: 1997-08-22
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87 EARLIER APPLICATION NUMBER: 60/056,909
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89 EARLIER APPLICATION NUMBER: 60/056,872
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 4 EARLIER APPLICATION NUMBER: 60/047,596
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 21 EARLIER FILING DATE: 1997-04-11
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 38 EARLIER APPLICATION NUMBER: 60/056,886
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 40 EARLIER APPLICATION NUMBER: 60/056,877
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 50 EARLIER APPLICATION NUMBER: 60/056,662
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 58 EARLIER APPLICATION NUMBER: 60/056,403
 59 EARLIER FILING DATE: 1997-08-22
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 68 EARLIER APPLICATION NUMBER: 60/056,911
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 70 EARLIER APPLICATION NUMBER: 60/056,616
 71 EARLIER FILING DATE: 1997-08-22
 72 EARLIER APPLICATION NUMBER: 60/056,874
 73 EARLIER FILING DATE: 1997-08-22

1 EARLIER APPLICATION NUMBER: 60/056,910
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 5 EARLIER APPLICATION NUMBER: 60/056,631
 6 EARLIER FILING DATE: 1997-08-22
 7 EARLIER APPLICATION NUMBER: 60/056,845
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 22 EARLIER FILING DATE: 1997-05-23
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 24 EARLIER FILING DATE: 1997-05-23
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 26 EARLIER FILING DATE: 1997-05-23
 27 EARLIER APPLICATION NUMBER: 60/047,589
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 40 EARLIER FILING DATE: 1997-08-22
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 42 EARLIER FILING DATE: 1997-08-22
 43 EARLIER APPLICATION NUMBER: 60/056,881
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 45 EARLIER APPLICATION NUMBER: 60/056,909
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 57 EARLIER APPLICATION NUMBER: 60/057,650
 58 EARLIER FILING DATE: 1997-09-05
 59 EARLIER APPLICATION NUMBER: 60/056,884
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 62 EARLIER FILING DATE: 1997-09-05
 63 EARLIER APPLICATION NUMBER: 60/049,610
 64 EARLIER FILING DATE: 1997-06-14
 65 EARLIER APPLICATION NUMBER: 60/061,060
 66 EARLIER FILING DATE: 1997-10-02

Alignment Scores:
 Pred. No.:

3,450,48

Length:

1142

Score: 476.50 Matches: 103
 Percent Similarity: 56.43% Conservativity: 55
 Best Local Similarity: 36.79% Mismatches: 97
 Query Match: 28.86% Indels: 25
 DB: 4 Gaps: 9

US-09-624-670-64 (1-299) x US-09-149 476 106 (1-1542)

QY 20 AspThrArgValLysGlyTrpPheLeuLeuAspAsnTyrIleProThrPheValCysSer 39
 DB 167 GAFCCCGGATCCAGGCTACCGCTGATGGGTC-----CCTTGGCTAATGACCTCC 220
 QY 40 ValIleTyrLeuLeuIleValTrp-----LeuGlyProLysTyrMetLysAsnArg 56
 DB 221 ATTCCTCCACCTAGCTGCTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 280
 QY 57 GlnProPheSerCysArgGlyIleLeuGlnLeuTyrAsnLeuGlyLeuThrLeuLeuSer 76
 DB 281 AAGCCCTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 340
 QY 77 LeuTyrMetPheTyrGlnLeuValThrGlyValTrpGluGlyLysTyrAsnPheCys 96
 DB 341 CTTACATGCTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 400
 QY 97 GlnGlyThrArgSerAlaGlyLeuSerAsp---MetLysIleIleArgValLeuTrpTrp 115
 DB 401 GACCTGCTGCTATTCACAGCCCTGAGCCTTAGGATGGTGGGCTGGCTGCTGCTGCTGCTGCT 460
 QY 116 TyrTyrPheSerLysLeuIleGluPheMetAspThrPhePheIleLeuArgLysAsn 135
 DB 461 TTTCT 520
 QY 136 AsnHisGlnIleThrValLeuHisValTyrHisHisAlaThrMetLeuAsnIleTrpTrp 155
 DB 521 GACGGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 580
 QY 156 PheValMetAsnTrpValProCysGlyHisSerTyrPheGlyAlaThrLeuAsnSerPhe 175
 DB 581 TGGGGGTAAAGATGGCCCGGAGGAATGGGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 640
 QY 176 IleHisValLeuMetTyrSerTyrTyrGlyLeuSerSerIle---ProSerMetArgPro 194
 DB 641 GTGCATGTCTATAGCTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 700
 QY 195 TyrLeuTrpTrpLysLysTyrIleThrGlnGlyGlnLeuValGlnPheValLeuThrIle 214
 DB 701 TACCTTTGGTGAAGAACGACATGACAGCCATTCAGCTGATCCAGTTTGTCTGCTCTCA 760
 QY 215 Ile-----GlnThrThrCysGlyValPheTrpProCysSerPhe 227
 DB 761 CTGCACATCTCCACTACTTTATGCTCCAGCTGCTAATACACAGTACCCAGTCATATT 820
 QY 228 ProLeuGlyTrpLeuPhePheGlnIleGlyTyrMetIleSerLeuIleAlaLeuPheThr 247
 DB 821 CACCTCATCTGATGATGGCACCATCTTCTCATG-----CTGTCTCC 865
 QY 248 AsnProTyrIleGlnThrTyrAsnLysGlyAlaSerArgArgLysAspHisLeuLys 267
 DB 866 AACTCTGTATCACTCTTATACCAAG-----GGCAAGCGGCTGCCCGCTGCACTTCAG 919
 QY 268 GlyHisGlnAsnGlySer-----ValAlaAlaValAsnGlyHisThrAsnSerPhePro 285
 DB 920 -----CAAAATGGAGCTCCAGGTATCCCAAGGCTCAAGGCTCAAGGCTCAAGGCTCAAGGCT 973

RESULT 3
 US-08-249-420-1
 : Sequence 1, Application US/08249420
 : Patent No 5484724
 : GENERAL INFORMATION:
 : APPLICANT: El-Sherbaili, Mohamed
 : APPLICANT: El-Sherbaili, Mohamed
 : TITLE OF INVENTION: DNA ENCODING GLS1
 : NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Christine E. Carty
 STREET: 126 E. Lincoln Avenue
 CITY: Rahway
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07055-0900
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/249,420
 FILING DATE: 26-May-1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Carty, Christine E.
 REGISTRATION NUMBER: 36,099
 REFERENCE/DOCKET NUMBER: 19162
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (908) 594-6734
 TELEFAX: (908) 594-4720
 INFORMATION FOR SEQ ID NO. 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1854 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-08-249-420-1

Alignment Scores:
 Pred. No.: 3,4e-30 Length: 1854
 Score: 326.50 Matches: 96
 Percent Similarity: 46.48% Conservativity: 56
 Best Local Similarity: 29.36% Mismatches: 128
 Query Match: 19.78% Indels: 47
 DB: 1 Gaps: 13

US-09-624-670-64 (1-299) x US-08-249-420-1 (1-1854)

QY 2 GlnHisPheAspAlaSerLeuSerThrTyrPheLysAlaPheLeuGlyProArgAspThr 21
 DB 715 GAACATTCGATGATGCTGCACCTGCTAATACAGGTAGATTGTTCCAACGCAATTC 774
 QY 22 Arg---ValLysGlyTrpPheLeuLeuAspAsnTyrIleProThrPheValCysSerVal 40
 DB 775 CAATTCATGCGAGTGAATACCATTAAGCACCTTGCCCTGCTGCTATAGCCATCACT 834
 QY 41 IleTyrLeuLeuIleValTrpLeuGlyProLysTyrMetLysAsnArgGlnProPheSer 60
 DB 835 GCCTATTACGTTATTTTGGTGGCAGGTTTGTAACTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAG 894
 QY 61 CysArgGlyIleLeuGlnLeuTyrAsnLeuGlyLeuThrLeuLeuSerLeuTyrMetPhe 80
 DB 895 ITAAATGGCCTTTTCCAATTCATAAATTTGGTTTAACTTCACTTTTCATTCAACGCTTTTA 954
 QY 81 TyrGluLeuValThrGly-----ValTrpGluGlyLysTyrAsnPhePhe 95
 DB 955 TTCTCTATGGTTGAACAATATTAGTGCATTTATTTGTCAGTACGGGTATATATCTGCTATC 1014
 QY 96 CysGlnGlyThrArgSerAlaGlyLeuSerAspMetLysIleIleArgValLeuTrpTrp 115
 DB 1015 TGT-----AATATTGCTGCTTGGCTCAACCGCTCGTTACATATTATATCATG 1063
 QY 116 TyrTyrPheSerLysLeuIleGluPheMetAspThrPhePheIleLeuArgLysAsn 135
 DB 1063 AATTACATTTGCAACTTTTATCAATTTATACACACCTTTTCTTGGTGTCTAATAA----- 1116
 QY 136 AsnHisGlnIleThrValLeuHisValTyrHisHis-----AlaThrMetLeuAsnIleTrp 154
 DB 1117 CATAAAAATGACATTTTTCATCATCTTATCACCATGGCTACTGCTTATATGTTAC 1176

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QY 155 TrpPheValMet ----- AsnTrpValProCysGlyHisSerTyrPheGly 169
DB 1177 ACCCAATGATGAGGACACAAATCATATTCTTGGTGGCTT ----- 1215
QY 170 AlaThrLeuAsnSerPheHisValLeuMetTyrSerTyrTyrGlyLeuSerSerIle 189
DB 1216 ATTTCATGAACCTGTCGTCACGTCGTCATGATGGTACATTTCTGGGTGCG --- 1272
QY 190 ProSerMetArgProTyrLeuTyrTrpTyrPheLeuThrGlnGlyLeuValGln 209
DB 1273 ACAGGATACAGT-----GCTGGTGGAGAGAAATGGGTACATTCCTAAATATCCAA 1326
QY 210 PheValLeu ----- ThrIleIleLeuInThrThrCysGlyValPhe 222
DB 1427 TTGTTTGGATATGTTTCATATATTTTGTCTGTACCAAAAAGACATTCCTTGAT 1386
QY 223 TrpPro ----- CysSerProLeuGlyTrpLeuPheGln 235
DB 1487 TTGCAATTTGGCAATTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1446
QY 246 IleGlyTyrMetIleSerLeuIleAlaLeuPheThrAsnPheTyrIleGlnThrTyrAsn 255
DB 1447 TGTGCAATATTTGTCATATTTGGTACATATTTTATTTTATTTTATTTTATTTTATA 1506
QY 256 LysGlyGlyAlaSerArgArgLysAspHisIleuLysGlyHisGlnAsnGlySerValAla 275
DB 1507 CGTAAGCGCAAAACACACAGTGTGTAAAGCTGGCCAC---GGGCTGTTCGCCGA 1563
QY 276 AlaValAsnGlyHisThrAsn----- SerProSerLeuGluAsnSerVal 291
DB 1564 AAGCTTAAATGACTATGTAACTGTTCACATCAAAAGCTTGGTACTCCATCTCCATCA 1623
QY 292 LysProArgLysGlnArgLys 298
DB 1624 AAACCTCAACACACACAAAA 1644

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RESULT 4
 US-08-747-663-1
 : Sequence 1, Application US-08/747663
 : Patent No. 5955347
 : GENERAL INFORMATION:
 : APPLICANT: El-Sherbini, Mohamed
 : APPLICANT: Clemas, Joseph
 : TITLE OF INVENTION: DNA ENCODING GLSI
 : NUMBER OF SEQUENCES: 2
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Joseph A. Coppola - MERCK & CO., INC.
 : STREET: 126 E. Lincoln Avenue - P.O. Box 2000
 : CITY: Rahway
 : STATE: New Jersey
 : COUNTRY: USA
 : ZIP: 07065
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent In Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US-08/737,664
 : FILING DATE:
 : CLASSIFICATION: 435
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US-08/249,420
 : FILING DATE: 26 MAY 1994
 : ATTORNEY/AGENT INFORMATION:
 : NAME: COPPOLA, JOSEPH A.
 : REGISTRATION NUMBER: 48,413
 : REFERENCE/DOCKET NUMBER: 19162PG
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 732 594 6744
 : TELEFAX: 732 594 4720
 : INFORMATION FOR SEQ 10 NO: 1:

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: SEQUENCE CHARACTERISTICS:  

: LENGTH: 1664 base pairs  

: TYPE: nucleic acid  

: STRANDEDNESS: single  

: TOPOLOGY: linear  

: MOLECULE TYPE: cDNA  

US-08-737-663-1

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Alignment Scores:  

Pred. No.: 8,4e-40 Length: 1664  

Score: 326.50 Matches: 96  

Percent Similarity: 46.48% Conservatvity: 56  

Best Local Similarity: 29.36% Mismatches: 128  

Query Match: 19.78% Indels: 47  

DB: 2 Gaps: 14

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US-09-624-670-64 (1 299) x US-08-747-663-1 (1 1854)

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QY 2 GluHisPheAspAlaSerLeuSerThrTyrPheLysAlaPheLeuGlyTyrArgAspThr 21
DB 715 GAACATTTCGATGATGTCGTCACGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 774
QY 22 Arg ValCysGlyTyrPheLeuLeuAspAsnTyrIleProThrPheValCysSerVal 40
DB 775 CAATTCATTCAGCGCAATTAACCAATTAAAGCACTTGGCTGGCTGGCTGGCTGGCT 834
QY 41 IleTyrLeuLeuValTyrLeuGlyProLysTyrMetLysAsnArgGlnProPheSer 60
DB 835 GCGTATTACGTTATTATTTTGGTGGCAGGTTTTTCTTAAGTAAGTCGGAACCATTTAAA 894
QY 61 CysArgGlyIleLeuGlnIleuTyrAsnLeuGlyLeuThrLeuLeuSerLeuTyrMetPhe 80
DB 895 TTAATGGCTTTTCCCAATTCGATATTTGGTTTAACTTCACTTCACTTCACTTCACTT 954
QY 81 TyrGlnLeuValThrGly ----- ValTrpGluGlyLysTyrAsnPhePhe 95
DB 955 TGGCTTAAGGTCGAACAAATAGTCGCAATATATGTTTACGACGAGTTATACTTCGCTAT 1014
QY 96 CysGlnGlyThrArgSerAlaGlyGluSerAspMetLysIleIleArgValLeuTyrTrp 115
DB 1015 TGT -----AATATTGGTGTGGACTCAACGCTGCTTACATATATATATACATG 1062
QY 116 TyrTyrPheSerLysLeuIleGluProMetAspPhePhePhePheLeuLeuArgLysAsn 145
DB 1063 AATTAATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1116
QY 136 AsnHisGlnIleThrValLeuHisValTyrHisHisAlaThrMetLeuAsnIleTyr 154
DB 1117 CATAAAAAATTCACATTTTTCGCAATTAACACATGCGGTACGCTTATTAATGTTAC 1176
QY 155 TrpPheValMet ----- AsnTrpValProCysGlyHisSerTyrPheGly 169
DB 1177 ACCCAATGATGAGGACACAAATCATATTCTTGGTGGCTT ----- 1215
QY 170 AlaThrLeuAsnSerPheHisValLeuMetTyrSerTyrTyrGlyLeuSerSerIle 189
DB 1216 ATTTCATGAACCTGTCGTCACGTCGTCATGATGGTACATTTCTGGGTGCG --- 1272
QY 190 ProSerMetArgProTyrLeuTyrTrpTyrPheLeuThrGlnGlyLeuValGln 209
DB 1273 ACAGGATACAGT-----GCTGGTGGAGAGAAATGGGTACATTCCTAAATATCCAA 1326
QY 210 PheValLeu ----- ThrIleIleLeuInThrThrCysGlyValPhe 222
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QY 223 TrpPro ----- CysSerProLeuGlyTrpLeuPheGln 235
DB 1487 TTGCAATTTGGCAATTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1446
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DB 1447 TGTGCAATATTTGTCATATTTGGTACATATTTTATTTTATTTTATTTTATTTTATA 1506
QY 256 LysGlyGlyAlaSerArgArgLysAspHisIleuLysGlyHisGlnAsnGlySerValAla 275
DB 1507 CGTAAGCGCAAAACACACAGTGTGTAAAGCTGGCCAC---GGGCTGTTCGCCGA 1563

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TITLE OF INVENTION: GENETICALLY ENGINEERING COTTON
TITLE OF INVENTION: PLANTS FOR ALTERED FIBER
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:

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1 TISSUE TYPE: fiber cells
2 IMMEDIATE SOURCE:
3 LIBRARY: CKFB10
4 CLONE: A11
5 US 08 530-797 6

Alignment Scores:
Pred. No.: 3,880-17 Length: 989
Score: 219.00 Matches: 56
Percent Similarity: 53.85% Conservatives: 35
Best Local Similarity: 33.14% Mismatches: 58
Query Match: 13.26% Indels: 20
DB: 1 Gaps: 7

US 09-624-670-64 (1 299) x US 08 530-797 6 (1 989)

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QY 115 Trp-----TyrTyrPheSerLysLeuIleGluPheMetAspThrPhePheLeu 131
DB 898 TGGGCAATACATCTCTTACCTTCCCAAGATTGTTGAAATCATGCAACCTTTTCATCATC 899

QY 132 LeuArgLysAsnAsuHisGlnIleThrValLeuHisValIleHisAlaThrMetLeu 151
DB 838 CTCAGCGGATCCATCAAGAGGTATGCTTCTTATGCTCATCATCATCATCATCATCATC 779

QY 152 AsuIleTrpPheValMetAsnTrpValProCysGlyHisSerTyrPheGlyAlaThr 171
DB 778 ATCATGCTTATATTTTATGATACACATGCTACTGCTGAGCAATGATGATGATGATGATC 719

QY 172 LeuAsnSerPheIleHisValLeuMetTyrSerTyrTyrLeuSerSerIleProSer 191
DB 718 --AACTGGCTGGTGAATGCTAAATGCTATGCTTATGCTGCTGCTGCTGCTGCTGCTG 665

QY 192 MetArgProCysGlyTrpPheValMetAsnTrpValProCysGlyHisSerTyrPheGlyAlaThr 211
DB 664 ATGACCCCAAGTGAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 611

QY 212 LeuThrIleGluThrTyrGlyValPheTrp-----ProCysSer 226
DB 610 TTAAGCTTTTGAATCAAGGCAATGCTGCTGCTTACACACACACACACACACACACACAC 551

QY 227 PheProLeuGlyTrpLeuPheGlnIleGlyTyrMetIleSerLeuIleAlaLeuPhe 246
DB 550 GGAATTCCTGATGATGCTCTTAAATGAGAGCTTAAAGCTGCTGCTGCTGCTGCTGCTGCTG 494

QY 247 ThrAsnPheTyrIleGluThrTyrAsn 255
DB 494 TCAGACTTTCATGCAAGAGTTACTCC 467

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RESULT 10

```

US 08 298-829 7/c
1 Sequence 7, Application US/08/298829
2 Patent No. 5620882
3 GENERAL INFORMATION:
4 APPLICANT: John, Malliyakal E.
5 TITLE OF INVENTION: GENETICALLY ENGINEERING COTTON
6 TITLE OF INVENTION: PLANTS FOR ALTERED FIBER
7 NUMBER OF SEQUENCES: 33
8 CORRESPONDENCE ADDRESS:
9 ADDRESSEE: Nicholas J. Seay, Charles & Ready
10 STREET: P.O. Box 2116, First Wisconsin Plaza
11 CITY: Madison
12 STATE: Wisconsin
13 COUNTRY: USA
14 ZIP: 53701
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE: Floppy disk
17 COMPUTER: IBM PC compatible
18 OPERATING SYSTEM: PC DOS/MS DOS
19 SOFTWARE: Microsoft Word

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1 CURRENT APPLICATION DATA:
2 APPLICATION NUMBER: US 08/298,829
3 FILING DATE: 19-OCT-1994
4 CLASSIFICATION: 800
5 PRIOR APPLICATION DATA:
6 APPLICATION NUMBER: US 07/885,970
7 FILING DATE: 18-MAY-1992
8 PRIOR APPLICATION DATA:
9 APPLICATION NUMBER: US 07/617,249
10 FILING DATE: 21-NOV-1990
11 PRIOR APPLICATION DATA:
12 APPLICATION NUMBER: US 07/253,243
13 FILING DATE: 04-OCT-1988
14 AUTOREY/AGENT INFORMATION:
15 NAME: Seay, Nicholas J.
16 REGISTRATION NUMBER: 27,486
17 TELECOMMUNICATION INFORMATION:
18 TELEPHONE: (608) 283-2478
19 TELEFAX: (608) 251-5139
20 INFORMATION FOR SEQ ID NO: 7:
21 SEQUENCE CHARACTERISTICS:
22 LENGTH: 989 base pairs
23 TYPE: nucleic acid
24 STRANDEDNESS: double
25 TOPOLOGY: linear
26 MOLECULE TYPE: cDNA
27 HYPOTHETICAL: NO
28 ANTI-SENSE: NO
29 ORIGINAL SOURCE:
30 ORGANISM: Gossypium hirsutum
31 STRAIN: Goker 312
32 DEVELOPMENTAL STAGE: 10 day old fiber cells
33 TISSUE TYPE: fiber cells
34 IMMEDIATE SOURCE:
35 LIBRARY: CKFB10
36 CLONE: A11
37 US 08 298-829-7

Alignment Scores:
Pred. No.: 3,880-17 Length: 989
Score: 219.00 Matches: 56
Percent Similarity: 53.85% Conservatives: 35
Best Local Similarity: 33.14% Mismatches: 58
Query Match: 13.26% Indels: 20
DB: 1 Gaps: 7

US 09-624-670-64 (1 299) x US 08 298 829-7 (1 989)

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QY 95 PhcysglnclgThrAlaGserAlaGlyGluSerAspMetLysIleLeuValLeuTrp 114
DB 937 TTCCCTAGGAGTACATGCTCCATCGGCCCTTCTCTTTTC 899

QY 115 Trp-----TyrTyrPheSerLysLeuIleGluPheMetAspThrPhePheLeu 131
DB 898 TGGGCAATACATCTCTTACCTTCCCAAGATTGTTGAAATCATGCAACCTTTTCATCATC 899

QY 132 LeuArgLysAsnAsuHisGlnIleThrValLeuHisValIleHisAlaThrMetLeu 151
DB 838 CTCAGCGGATCCATCAAGAGGTATGCTTCTTATGCTCATCATCATCATCATCATCATC 779

QY 152 AsuIleTrpPheValMetAsnTrpValProCysGlyHisSerTyrPheGlyAlaThr 171
DB 778 ATCATGCTTATATTTTATGATACACATGCTACTGCTGAGCAATGATGATGATGATGATC 719

QY 172 LeuAsnSerPheIleHisValLeuMetTyrSerTyrTyrLeuSerSerIleProSer 191
DB 718 --AACTGGCTGGTGAATGCTAAATGCTATGCTTATGCTGCTGCTGCTGCTGCTGCTG 665

QY 192 MetArgProCysGlyTrpPheValMetAsnTrpValProCysGlyHisSerTyrPheGlyAlaThr 211
DB 664 ATGACCCCAAGTGAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 611

QY 212 LeuThrIleGluThrTyrGlyValPheTrp-----ProCysSer 226

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DB      610 TTAAGCTTTTGAATAGGAGLAAAGCTTGTTGTTCTACCACTTCACCTCCCTTCGGCGTCTCT 551
QY      227 PheProLeuGlyTrpLeuPheGlnIleGlyTyrMetIleSerLeuIleAlaLeuPhe 246
DB      550 GGGATTCTGATTTGGTGT---TTCAATGAGAGCTTCAAGGTCCTCTCTCTACTTGTTC 494
QY      247 ThrAsnPheTyrIleGlnThrTyrAsn 255
DB      493 TCAGACTTTTCAATGCAAGAATTACTGC 467

RESULT 11
: US-08-787-335-6/c
: Sequence 6, Application US/08787335
: Patent No. 5981834
: GENERAL INFORMATION:
: APPLICANT: John, Maliyakal E.
: APPLICANT: Umbeck, Paul F.
: APPLICANT: Brill, Winston J.
: TITLE OF INVENTION: GENETICALLY ENGINEERED COTTON PLANTS
: NUMBER OF SEQUENCES: 18
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Quarles and Brady
: STREET: P.O. BOX 2113
: CITY: FIRST WISCONSIN PLAZA
: STATE: MADISON
: COUNTRY: U.S.A.
: ZIP: 53701
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette - 3.50 inch, 800kb storage
: COMPUTER: Apple Macintosh
: OPERATING SYSTEM: Macintosh
: SOFTWARE: Microsoft Word 4.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/787,335
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/530,797
: FILING DATE:
: APPLICATION NUMBER: 04-OCT-88
: FILING DATE: 04-OCT-88
: ATTORNEY/AGENT INFORMATION:
: NAME: Nicholas J. Seay
: REGISTRATION NUMBER: 27,386
: REFERENCE/DOCKET NUMBER: 1122990245
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 989 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA to mRNA
: HYPOTHETICAL: no
: ANTI-SENSE: no
: ORIGINAL SOURCE:
: ORGANISM: Gossypium hirsutum
: STRAIN: Coker 312
: DEVELOPMENTAL STAGE: 10 day old fiber cells
: TISSUE TYPE: fiber cells
: IMMEDIATE SOURCE:
: LIBRARY: CKB10
: CLONE: All
: US-08-787-335-6

Alignment Scores:
Pred. No.: 3 88e-17 Length: 989
Score: 219.90 Matches: 56
Percent Similarity: 53.8% Conservative: 35
Best Local Similarity: 33.14% Indels: 58
Query Match: 13.26% Indels: 20

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DB      95 PheCysGlnGlyThrArgSerLagIleGluSerAspMetLysIleAlaValLeuTrp 114
DB      937 TTCCTTAGGGGTACATCCCATCGGCGCT---CTCTTTTC 899
QY      115 Ttp-----TyrTyrPheSerLysLeuIleGluPheMetAspThrPhePhePheIle 131
DB      898 TGGGCATACATCTCTACCTCTCCAGATTGTGAATTCATGACACCCCTTTTGTATCATC 839
QY      132 LeuAtgLysAsnAsnHisGlnIleThrValLeuHisValTyrHisHisAlaThrMetLeu 151
DB      838 CTCAGCGGATCATGAAGAGGTATCTCTCTTACGCTACCATCATCGTGTGTC 779
QY      152 AsnIleTrpTrpPheValMetAsnTrpValProCysGlyHisSerTyrPheGlyAlaThr 171
DB      778 ATCATGTGTATATTTCCTTAGACAGTCTCAGTCTCCGACCATGGTCTGTCATCAC 719
QY      172 LeuAsnSerPheIleHisValLeuMetTyrSerTyrTyrGlyLeuSerSerIleProSer 191
DB      718 ---AACTGCTGTGTCATGCTGAATGACTCTTACTCTATTACTGTTGTGCACCTG---GGG 665
QY      194 MetArgProTyrLeuTrpTrpLysLysTyrIleThrGlyGlnLeuValGlnPheVal 211
DB      664 ATGCACCCCAAG-----TGAAGAAATGGTGACGGATTTCACACTGGTGCAGTCCGG 611
QY      212 LeuThrIleIleGlnThrThrCysGlyValPheTrp-----ProCysSer 226
DB      610 TTAAGCTTTTTCATCATGCCCATGCTGTGTGTTCTACCACTTCACCTGCTTCTGCTCTCT 551
QY      227 PheProLeuGlyTrpLeuPheGlnIleGlyTyrMetIleSerLeuIleAlaLeuPhe 246
DB      550 GGGATTCTGATTTGGTGT---TTCAATGAGAGCTTCAAGGTCCTCTCTCTACTTGTTC 494
QY      247 ThrAsnPheTyrIleGlnThrTyrAsn 255
DB      493 TCAGACTTTTCAATGCAAGAATTACTGC 467

RESULT 12
: US-09-145-828A-5
: Sequence 9, Application US/09145828A
: Patent No. 6403349
: GENERAL INFORMATION:
: APPLICANT: Abbott Laboratories
: APPLICANT: Mukerji, Pradip
: APPLICANT: Leonard, Amanda E. Y.
: APPLICANT: Fuang, Yung-Sheng
: APPLICANT: Thurmond, Jennifer
: APPLICANT: Kirchner, Stephen J.
: APPLICANT: Farber-Barnes, Jennifer M.
: TITLE OF INVENTION: THE ELONGASE GENE AND USES THEREOF
: FILE REFERENCE: 6407.US.01
: CURRENT APPLICATION NUMBER: US/09/145,828A
: CURRENT FILING DATE: 1998-09-02
: NUMBER OF SEC ID NOS: 30
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 9
: LENGTH: 587
: TYPE: DNA
: ORGANISM: Mortierella alpina
: US-09-145-828A-9

Alignment Scores:
Pred. No.: 2 85e-16 Length: 587
Score: 209.00 Matches: 58
Percent Similarity: 49.50% Conservative: 42
Best Local Similarity: 28.71% Mismatches: 66
Query Match: 12.66% Indels: 36
DB: 4 Gaps: 10

US-09-624-670-64 (1-299) x US-09-145-828A-9 (1-587)

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1	EARLIER APPLICATION NUMBER: 60/047,598	1	EARLIER FILING DATE: 1997-08-22	1	EARLIER FILING DATE: 1997-08-22
2	EARLIER FILING DATE: 1997-05-23	2	EARLIER APPLICATION NUMBER: 60/056,874	2	EARLIER FILING DATE: 1997-08-22
3	EARLIER APPLICATION NUMBER: 60/047,613	3	EARLIER FILING DATE: 1997-08-22	3	EARLIER FILING DATE: 1997-08-22
4	EARLIER FILING DATE: 1997-05-23	4	EARLIER APPLICATION NUMBER: 60/056,910	4	EARLIER FILING DATE: 1997-08-22
5	EARLIER APPLICATION NUMBER: 60/047,582	5	EARLIER FILING DATE: 1997-08-22	5	EARLIER FILING DATE: 1997-08-22
6	EARLIER FILING DATE: 1997-05-23	6	EARLIER APPLICATION NUMBER: 60/056,864	6	EARLIER FILING DATE: 1997-08-22
7	EARLIER APPLICATION NUMBER: 60/047,596	7	EARLIER FILING DATE: 1997-08-22	7	EARLIER FILING DATE: 1997-08-22
8	EARLIER FILING DATE: 1997-05-23	8	EARLIER APPLICATION NUMBER: 60/056,631	8	EARLIER FILING DATE: 1997-08-22
9	EARLIER APPLICATION NUMBER: 60/047,612	9	EARLIER FILING DATE: 1997-08-22	9	EARLIER FILING DATE: 1997-08-22
10	EARLIER FILING DATE: 1997-05-23	10	EARLIER APPLICATION NUMBER: 60/056,845	10	EARLIER FILING DATE: 1997-08-22
11	EARLIER APPLICATION NUMBER: 60/047,632	11	EARLIER FILING DATE: 1997-08-22	11	EARLIER FILING DATE: 1997-08-22
12	EARLIER FILING DATE: 1997-05-23	12	EARLIER APPLICATION NUMBER: 60/056,892	12	EARLIER FILING DATE: 1997-08-22
13	EARLIER APPLICATION NUMBER: 60/047,601	13	EARLIER FILING DATE: 1997-08-22	13	EARLIER FILING DATE: 1997-08-22
14	EARLIER FILING DATE: 1997-05-23	14	EARLIER APPLICATION NUMBER: 60/057,761	14	EARLIER FILING DATE: 1997-08-22
15	EARLIER APPLICATION NUMBER: 60/043,580	15	EARLIER FILING DATE: 1997-08-22	15	EARLIER FILING DATE: 1997-08-22
16	EARLIER FILING DATE: 1997-04-11	16	EARLIER APPLICATION NUMBER: 60/047,595	16	EARLIER FILING DATE: 1997-05-23
17	EARLIER APPLICATION NUMBER: 60/043,568	17	EARLIER FILING DATE: 1997-05-23	17	EARLIER APPLICATION NUMBER: 60/047,599
18	EARLIER FILING DATE: 1997-04-11	18	EARLIER FILING DATE: 1997-05-23	18	EARLIER APPLICATION NUMBER: 60/047,588
19	EARLIER APPLICATION NUMBER: 60/043,314	19	EARLIER FILING DATE: 1997-05-23	19	EARLIER FILING DATE: 1997-05-23
20	EARLIER FILING DATE: 1997-04-11	20	EARLIER APPLICATION NUMBER: 60/047,586	20	EARLIER FILING DATE: 1997-05-23
21	EARLIER APPLICATION NUMBER: 60/043,569	21	EARLIER FILING DATE: 1997-05-23	21	EARLIER FILING DATE: 1997-05-23
22	EARLIER FILING DATE: 1997-04-11	22	EARLIER APPLICATION NUMBER: 60/047,590	22	EARLIER FILING DATE: 1997-05-23
23	EARLIER APPLICATION NUMBER: 60/043,311	23	EARLIER FILING DATE: 1997-05-23	23	EARLIER FILING DATE: 1997-05-23
24	EARLIER FILING DATE: 1997-04-11	24	EARLIER APPLICATION NUMBER: 60/047,594	24	EARLIER FILING DATE: 1997-05-23
25	EARLIER APPLICATION NUMBER: 60/043,671	25	EARLIER FILING DATE: 1997-05-23	25	EARLIER APPLICATION NUMBER: 60/047,589
26	EARLIER FILING DATE: 1997-04-11	26	EARLIER FILING DATE: 1997-05-23	26	EARLIER FILING DATE: 1997-05-23
27	EARLIER APPLICATION NUMBER: 60/043,674	27	EARLIER FILING DATE: 1997-05-23	27	EARLIER FILING DATE: 1997-05-23
28	EARLIER FILING DATE: 1997-04-11	28	EARLIER APPLICATION NUMBER: 60/047,594	28	EARLIER FILING DATE: 1997-05-23
29	EARLIER APPLICATION NUMBER: 60/043,669	29	EARLIER FILING DATE: 1997-05-23	29	EARLIER APPLICATION NUMBER: 60/047,593
30	EARLIER FILING DATE: 1997-04-11	30	EARLIER FILING DATE: 1997-05-23	30	EARLIER FILING DATE: 1997-05-23
31	EARLIER APPLICATION NUMBER: 60/043,312	31	EARLIER FILING DATE: 1997-05-23	31	EARLIER FILING DATE: 1997-05-23
32	EARLIER FILING DATE: 1997-04-11	32	EARLIER APPLICATION NUMBER: 60/047,593	32	EARLIER FILING DATE: 1997-05-23
33	EARLIER APPLICATION NUMBER: 60/043,313	33	EARLIER FILING DATE: 1997-05-23	33	EARLIER FILING DATE: 1997-05-23
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35	EARLIER APPLICATION NUMBER: 60/043,672	35	EARLIER FILING DATE: 1997-05-23	35	EARLIER FILING DATE: 1997-05-23
36	EARLIER FILING DATE: 1997-04-11	36	EARLIER APPLICATION NUMBER: 60/043,578	36	EARLIER FILING DATE: 1997-04-11
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40	EARLIER FILING DATE: 1997-06-06	40	EARLIER APPLICATION NUMBER: 60/047,501	40	EARLIER FILING DATE: 1997-05-23
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42	EARLIER FILING DATE: 1997-08-22	42	EARLIER APPLICATION NUMBER: 60/043,670	42	EARLIER FILING DATE: 1997-04-11
43	EARLIER APPLICATION NUMBER: 60/056,877	43	EARLIER FILING DATE: 1997-04-11	43	EARLIER FILING DATE: 1997-08-22
44	EARLIER FILING DATE: 1997-08-22	44	EARLIER APPLICATION NUMBER: 60/056,632	44	EARLIER FILING DATE: 1997-08-22
45	EARLIER APPLICATION NUMBER: 60/056,889				

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 Score: 138.50 Matches: 28
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 Best Local Similarity: 45.00% Mismatches: 30
 Query Match: 8.40% Indels: 5
 DB: 4 Gaps: 2

US-09-624-670-64 (1 299) x US-09-624-670-64 (1 844)

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 DB 94 CATCCCGGATCCAGAGGCTACCCCTCATGCGGTC-----CCCTCTTAATGACCTCC 147
 QY 40 ValletYrLeuLeuLeuValTrp-----LeuGlyProLysTyrMetLysAsnArg 56
 DB 148 ATTCCTCAGCTACGCTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 207
 QY 57 GluProPheSorCysArqGlyLleLeuGlnLeuLysLeuGlyLeuLysLeuLeuSor 76
 DB 208 AAGGCTTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 267
 QY 77 LeuTyrMetPheTyrGluLeuValThrGlyValTrpGluGlyLysTyrAsnProPheCys 96
 DB 268 CTTACATCTCTATGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 327

RESULT 15

US-09-624-670-64 (1 299) x US-09-624-670-64 (1 844)

Sequence 3: Application US/04464461B

Patent No.: 5981178

GENERAL INFORMATION:

APPLICANT: Tsui, Lap Chee

APPLICANT: Pommers, Johanna M.

APPLICANT: Kerem, Bat Sheva

TITLE OF INVENTION: Introns and Exons of the Cystic Fibrosis Gene and

Mutations at Various Positions of the Gene

FILE REFERENCE: 3477-61, 634477/139840

CURRENT APPLICATION NUMBER: US/04464461B

CURRENT FILING DATE: 1995-06-06

NUMBER OF SEQ ID NOS: 43

SOFTWARE: Patent In Ver. 2.0

SEQ ID NO 3

LENGTH: 22846

TYPE: DNA

ORGANISM: Homo sapiens

US-09-624-670-64 (1 299) x US-09-624-670-64 (1 844)

Alignment Scores:

Pred. No.: 1,835 Length: 22846
 Score: 100.50 Matches: 54
 Percent Similarity: 46.57% Conservativeness: 44
 Best Local Similarity: 20.15% Mismatches: 89
 Query Match: 6.09% Indels: 81
 DB: 2 Gaps: 13

US-09-624-670-64 (1 299) x US-09-624-670-64 (1 22846)

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 QY 44 ProThrPheValCysSorValLleTyrLeuLeuLleValTrpLeuGlyProLysTyrMet 53
 DB 15347 -----ATTTCGATATGATATTCATTAATTCATTTCTTCAGGTCACAGATATAT 15497
 QY 54 LysAsnArgLlnProPheSorCysArqGlyLleLeuGlnLeuLeuLysLeuGlyLeuSor 73
 DB 15398 GAAAT- -----TACATTTTGTTTATGT 15421
 QY 74 LeuLeuSerLeuTyrMet-----PheTyrGluLeu 83
 DB 15422 TATTGCAATGTTTCTTATGCAAAATTTTCACAGGACGCAATTTTCATCATGCT 15481

QY 84 ValThr-----GlyValTrpGlu-----GlyLysTyrAsnProPheCys 96
 DB 15482 GTTCAAGCTTAAAGAGCTATGAGCACTTGCTGCGCTGAGAGGAGGCTTACTTT 15538
 QY 97 GluGlyThrArgSerAlaGlyGluSorAspMetLysLleLeuValLeuTrpTrpTyr 116
 DB 15539 -----GAACTCTGCTCCACAAAGTCTGAAATTAATATACCTGCACTGCTCTTC 15589
 QY 117 TyrPheSerLysLeu-----ThrGluPheMetAspThrPhePhePhe 130
 DB 15590 TACCTGTCACACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 15649
 QY 131 IleLeuArgLysAsnAsnHisGlnLleThrValLeuHisValTyrHisHisAlaThrMet 150
 DB 15650 ATT-----GCTGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 15691
 QY 151 LeuAsnLleTrpTrpPheValMetAsnTrpValProCysGlyHisSerTyrPheGlyAla 170
 DB 15692 AACCTCACTA-----ACCTTACCTAAACATTAACATAAAATTT 15740
 QY 171 ThrLeuAsnSerPheIleHisValLeuMetTyrSerTyrTyrLeuLeuSerSerIlePro 190
 DB 15731 TCAATCAATAAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 15784
 QY 191 SerMetArgProTyrLeuTrpTrpLysTyrIleThrGlnGlyGlnLeuValGlnPhe 210
 DB 15785 TTTAGTAATTAAACAAATTTGTTGG-----TTTATTATTGAAACAA 15823
 QY 211 ValLeuThrIleLleGlnThrThrCysGlyValPheThrProCysSerPheProLeuGly 240
 DB 15824 GTCAATTTCTTTG-----AAATTTCAATTTGTTT 15850
 QY 231 TrpLeu-----PhePheGlnIleGlyTyrMetIleSerLeuLleAlaLeuPhe 246
 DB 15851 TATGTTTAAACAAATAATTTGCTTGAATCGGATATAATAATAATATATATATATAT 15910
 QY 247 ThrAsnProTyrIleGlnThrTyr 254
 DB 15911 AT 15944

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Job time : 67.6396 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd

OM protein - nucleic search, using frame_plus_2a model

Run on: June 15, 2003, 23:02:06 ; Search time 131.034 seconds

(without alignments)
3304.262 Million cell updates/sec

Title: US-09-624-670-64

Perfect score: 1651

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Xgapop 10.0, Xgapext 0.5

fgapop 6.0, fgapext 7.0

delop 6.0, delext 7.0

Searched: 102988 seqs, 7240303 residues

Total number of hits satisfying chosen parameters 205976

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTPMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=us09624670 -XN1=1 -XN2=1 -XN3=1 -XN4=1 -XN5=1 -XN6=1 -XN7=1 -XN8=1 -XN9=1 -XN10=1
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-FGAPOP=6 -FGAPEXT=7 -XGAPOP10=5 -DELOP=6 -DELEXT=7

Database :

Published Applications_NA:*

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8: /cgn2_6/ptodata/1/pubpna/us08_purcOMB.seq.*
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1651	100.0	900	10	us-09-903-456-6
2	1558	94.4	914	10	us-09-903-456-3
3	1108	67.1	871	9	us-09-764-888-453
4	1089	64.7	748	9	us-09-764-888-352

5	956.5	57.9	879	9	US-09-849-199A-22
6	956.5	57.9	879	10	US-09-903-456-5
7	954.5	57.8	2426	9	US-10-138-846-13406
8	724	43.9	2225	10	US-09-925-301-248
9	548	33.2	384	9	US-09-918-995-37438
10	452	29.8	430	9	US-09-918-995-17480
11	476.5	28.9	1482	9	US-09-809-391-258
12	476.5	28.9	1542	9	US-09-809-391-106
13	445	27.0	1682	10	US-09-822-830A-345
14	395.5	24.0	819	10	US-09-903-456-7
15	395.5	24.0	819	10	US-09-903-456-72
16	391.5	23.7	819	10	US-09-903-456-73
17	390.5	23.7	819	10	US-09-903-456-70
18	388.5	23.5	818	10	US-09-903-456-71
19	386.5	23.4	819	10	US-09-903-456-69
20	385.5	23.3	819	10	US-09-903-456-74
21	381.5	23.1	957	10	US-09-903-456-2
22	358	21.7	549	9	US-09-911-936-1727
23	332	20.1	196	10	US-09-864-761-19026
24	332	20.1	212	10	US-09-864-761-26863
25	332	20.1	409	10	US-09-864-761-33069
26	332	20.1	485	10	US-09-864-761-2289
27	332	20.1	8861	9	US-09-764-868-1445
28	328	19.9	455	10	US-09-864-761-10225
29	294	17.8	630	10	US-09-903-456-67
30	276.5	16.7	447	9	US-09-918-995-9957
31	260	15.7	24664	9	US-10-073-961-613
32	260	15.7	24664	10	US-09-764-887-613
33	255	15.4	590	10	US-09-903-456-17
34	249	15.1	954	10	US-09-903-456-1
35	246.5	14.9	867	10	US-09-903-456-4
36	232	14.1	1387	9	US-10-138-846-12745
37	227	13.7	2775	9	US-10-161-521A-3
38	227	13.7	2989	9	US-09-759-130B-221
39	217	13.1	795	9	US-09-759-130B-222
40	217	13.1	798	10	US-09-903-456-63
41	216	13.1	813	9	US-09-759-130B-238
42	209	12.7	587	10	US-09-903-456-16
43	209	12.7	167	10	US-09-783-590-46
44	189	10.4	512	9	US-09-918-995-40797
45	164	9.9	470	9	US-09-918-995-968

ALIGNMENTS

RESULT 1
US-09-903-456-6
Sequence 5, Application US/09093456
Protect No. US20020138874A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pradip
APPLICANT: Leonard, Amanda Eun-Yeong
APPLICANT: Huang, Yung-Sheng
APPLICANT: Pereira, Suzette L.
TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
FILE REFERENCE: 6407.US.P3
CURRENT APPLICATION NUMBER: US/09/903.456
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: US 09/624,670
PRIOR FILING DATE: 2000-07-24
PRIOR APPLICATION NUMBER: US 09/379,095
PRIOR FILING DATE: 1999-08-23
PRIOR APPLICATION NUMBER: US 09/145,828
PRIOR FILING DATE: 1998-09-02
NUMBER OF SEQ ID NOS: 116
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 6
LENGTH: 900
TYPE: DNA
ORGANISM: Mus musculus
US-09-903-456-6

Alignment Scores:

Pred. No.: 1,2e-101 Length: 879
 Score: 956.50 Matches: 168
 Percent Similarity: 71.58% Conservatively: 36
 Best Local Similarity: 58.95% Mismatches: 78
 Query Match: 57.93% Indels: 3
 DB: 10 Gaps: 1

US-09-624-670-64 (1-299) x US-09-903-456-5 (1-879)

```

QY 1 MetGluHisValSerLeuSerThrTyrPheLysAlaPheLeuGlyProAsp 20
DB 10 CTGAAGGCTTGTGATTAATGTTTATGGAACAAAGTTTGAACAGAGAT 54
QY 2 ThrArgValLysGlyTrpPheLeuAspSerVal 40
DB 70 TCTGAGTCGGGGTGGTTCCTGGACCTTACCTCCACCTTCACTCCACCATC 129
QY 41 IleTyrLeuLeuValTrpLeuGlyProLysTyrMetLysAsnArgGlnProPheSer 60
DB 130 AGCTACCTGCTCTGCAATAGGGCTGGIAACAAGATACAGAAGAACAGGCTGCTGCT 189
QY 61 CysArgGlyLleLeuGlnLeuTyrAsnLeuGlyLeuThrLeuSerLeuTyrMetPhe 80
DB 190 ATGAGAGATGCTATTTGATTAATCTCGCAATCACTCTTTTACGATATATGCTG 249
QY 81 TyrGluLeuValThrGlyValTrpGlyLysTyrAsnPheCysGlnGlyThrArg 100
DB 250 GTGGAGCTCATCTCTCCAGCTGGAGAGAGGTTACAACTTGCAGTGTCAAGATCTCGAC 309
QY 101 SerAlaGlyGluSerAspMetLysIleIleArgValLeuTrpTyrPheSerLys 120
DB 310 ACTGAGGAGAGAGTGAAGTGGGTGAGTGAAGGTCCTGGTGGTACTACTCTCCAAA 359
QY 121 LeuIleGluPheMetAspThrPhePhePheIleLeuArgLysAsnAsnHisGlnIleThr 140
DB 370 CTATGGAGTTCTGCGACAGCATTTCTTTCTAGCAAAAAAGACAAATCAGATCAAC 429
QY 141 ValIleHisValTyrHisAlaThrMetLeuAsnIleTrpTrpPheValMetAsnTrp 160
DB 430 TTCCCTTCAGTGTATACACACCGGCCATGTTCACATCTGGTGGTGTGTGTAACCTGG 489
QY 161 ValProCysGlyHisSerTyrPheGlyAlaThrLeuAsnSerPheIleHisValLeuMet 180
DB 490 ATACCTTGTGTCFAAAGCTCTTTGGACCCACCTGAACAGCTTATCCACATCTCATC 549
QY 181 TyrSerTyrGlyLeuSerSerIleProSerMetArgProTyrLeuValTyrTrpLysLys 200
DB 550 TACTCTACTACAGATTTTGTGTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 609
QY 201 TyrIleThrGlnGlyAlaLeuValGlnPheValIleThrIleIleGlnThrThrCysGly 220
DB 610 IACCTCACACAGATGACAGTGGGACGTTGCTACTATACACAGATGACAGTGGC 659
QY 221 ValPheTrpProCysSerPheProLeuGlyTrpLeuPheGluGlyTyrMetIle 240
DB 670 GTGGTCAACCTCTGGCTTCCCTTGGCTGCTCACTCCAGCTTCCATATATGATG 729
QY 241 SerLeuIleAlaLeuPheThrAsnPheTyrIleGlnThrTyrAsnLysLysGlyAlaSer 260
DB 730 AGCTAGTATATGTTTAAATTTCTATATCAGATATACAGGAAAGAGAGAGAGAG 789
QY 261 Arg-----ArgLysAspHisLeuLysGlyHisGlnAsnGlySerValAlaAlaVal 277
DB 790 AAACAGCTTCCAGACAGACAGATTAATATGTTTCCCAAAAGGCTATTAATTTGGGCT 849
QY 278 AsnGlyHisThrAsn 282
DB 850 AATGGCAATCAGCGAC 864

```

RESULT 7

US-10-198-846-13406

: Sequence 13406, Application US/10198846

Publication No. US20030094974A1
 GENERAL INFORMATION:
 APPLICANT: Billie, James
 APPLICANT: Xu, Yongyao
 APPLICANT: Wang, Youzhen
 APPLICANT: Steinmann, Kathleen
 TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
 FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
 THERAPY OF BREAST CANCER
 FILE REFERENCE: MRI-049
 CURRENT APPLICATION NUMBER: US/10/198,846
 PRIOR FILING DATE: 2003-07-18
 PRIOR APPLICATION NUMBER: 60/306,220
 PRIOR FILING DATE: 2001-07-18
 NUMBER OF SEQ ID NOS: 14084
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 13406
 LENGTH: 2425
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc.feature
 LOCATION: 1, 2425, 2425
 OTHER INFORMATION: n = A,T,C or G
 US-10-198-846-13406

Alignment Scores:

Pred. No.: 9,79e-101 Length: 2426
 Score: 954.50 Matches: 173
 Percent Similarity: 70.47% Conservatively: 37
 Best Local Similarity: 58.05% Mismatches: 81
 Query Match: 57.81% Indels: 7
 DB: 9 Gaps: 3

US-09-624-670-64 (1-299) x US-10-198-846-13406 (1-2426)

```

QY 1 MetGluHis-----PheAspAlaSerLeuSerThrTyrPheLysAlaPheLeuGly 17
DB 85 ATGGAAACATCTAAAGCCCTTTGATGATGAAATCAATGCTTTTGGACAATATGTTGGA 144
QY 18 ProArgAspThrArgValLysGlyTrpPheLeuLeuAspAsnTyrIleProThrPheVal 37
DB 145 CAGTGGAGATTCCTCGAGTCAGAGGTGGTTCACTGTGGACTGTTACCTTCCTACCTTTT 204
QY 38 CysSerValIleTyrLeuLeuValTrpLeuGlyProLysTyrMetLysAsnArgGln 57
DB 205 CTTACTGTGATGATGCTGCTCTCAAAATGGGCTGGGTAACAAAGTATATGAAGACAGCT 264
QY 58 ProPheSerCysArgGlyIleLeuGlnLeuTyrAsnLeuGlyLeuThrLeuLeuSerLeu 77
DB 265 GCTCTTTCTCTCAGGGGTATCTCACCCTGTATATCTTGAATCAGACTTCTCTCGCG 324
QY 78 TyrMetPheTyrGluLeuValThrGlyValTrpGlyLysTyrAsnPhePheCysGln 97
DB 325 TACATGTTGGAAGACTTATCTCTACATTTGGGAGAGAGCTTCAACTTACAGTGTCAA 384
QY 98 GlyThrArgSerAlaGlyGluSerAspMetLysIleIleArgValLeuTrpTrpTyr 117
DB 385 CATCTTACCGCGCAGCGGAAAGCTCACATCGGCTAGGAGTGTCTTGGTGTCTACTAT 444
QY 118 PheSerLysLeuIleGluPheMetAspThrPhePhePheIleLeuArgLysAsnAsnHis 137
DB 445 TTCTCCAAATCAGTAGAGTTCTCGACACAAATTTCTCTTTTGGCGAAAAAACAGT 504
QY 138 GlnIleThrValLeuHisValTyrHisHisAlaThrMetLeuAsnIleTrpTrpPheVal 157
DB 505 CAGATTACTTTTCTTCATGATATCATCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 564
QY 158 MetAsnTrpValProCysGlyHisSerTyrPheGlyAlaThrLeuAsnSerPheIleHis 177
DB 565 TTGAACCTGGAACCTTGTGGACAAAGTTTCTTGGACCAACACTTGAACACTTATATCCAC 624
QY 178 ValLeuMetTyrSerTyrGlyLeuSerSerIleProSerMetArgProTyrLeuTrp 197

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Db      625 ATTCCTATGACACGCTACATGAGCACTTCCTGCTTCCATCATCATGACACAGTATCTTGG 684
QY      198 TrpLysLysTyrIleThrGlnGlnGlnLeuValGlnPheValLeuThrIleLeuGlnThr 217
Db      685 TCGAAGAAATATGCTACACAGCTGCTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 744
QY      218 ThrCysGlyValPheThrProCysSerPheProLeuGlyTrpLeuPheGlnIleGly 237
Db      745 ATGACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 804
QY      248 TyrMetIleSerLeuIleAlaLeuPheThrAsnPheThrIleGlnThrTyrAsnLysLys 257
Db      805 TATATGCTAAGCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 864
QY      258 GlyAlaSerArgAlaLeuAspHisLeuLysGlyHisLeuLysGlyHisLeuLysGlyHis 277
Db      865 -- --CCAAATGCAAAAGATATGCAAGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 912
QY      278 AsnGlyHisThrAsnGlyPheProSerLeuGluAspSerValLysProArgLys 295
Db      913 AATGCTTTTTCGAAAGCTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 966

RESULT 8
US-09-925-301-248
: Sequence 248, Application US/09/25301
: Patent No. US20020052308A1
: GENERAL INFORMATION:
: APPLICANT: Rosed et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
: FILE REFERENCE: PAL06
: CURRENT APPLICATION NUMBER: US/09/925,301
: CURRENT FILING DATE: 2001-08-10
: PRIOR APPLICATION NUMBER: PCT/US00/06982
: PRIOR FILING DATE: 2000-03-08
: PRIOR APPLICATION NUMBER: 69/124,270
: PRIOR FILING DATE: 1999-03-12
: NUMBER OF SEQ ID NOS: 1694
: SEQ ID NO 248
: LENGTH: 2225
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (14)
: OTHER INFORMATION: n equals a.t.g. or c
US-09-925-301-248

Alignment Scores:
Pred. No.: 5,826-74 Length: 2225
Score: 724.00 Matches: 133
Percent Similarity: 90.97% Conservative: 8
Best Local Similarity: 85.81% Mismatches: 5
Query Match: 43.85% Indels: 9
Db: 10 Gaps: 1

US-09-624-670-64 (1-299) x US-09-925-301-248 (1-2225)
QY      146 HISHSALATHMOTLEUASNLIEITPTTPPHEVALMETASNLTPVALPROCYSLYHS 165
Db      31 CACCATGCTGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 66
QY      166 SerTyrPheGlyAlaThrLeuAspSerPheIleHisValLeuMetTyrSerTyrTyrGly 185
Db      67 TCTATTATTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 124
QY      186 LeuSerSerIleProSerMetArgProTyrLeuTrpIleLysLysTyrIleThrGlnGln 205
Db      127 TTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 146
QY      205 yGlnGlnValGlnPheValLeuThrIleIleLeuThrThrCysGlyValPheThrProCys 225

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Db      147 GCACCTGCTTCACGCTTCGCTGACAAATATATCAATAGTTCGGGAGTTCGCTG 246
QY      225 sSerPheProLeuGlyTrpLeuPhePheGlnIleGlyTyrMetIleSerLeuIleAlaLeu 245
Db      247 CACATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 406
QY      245 uPheThrAsnPheThrIleGlnThrTyrAsnLysLysLysValAspSerValAlaLeuLysAspHis 265
Db      307 CTTCATCAAAATTTCTATATATAGACCTATCAACCAAGAAAAGGGGCTTCGGGAAGGAAGCA 466
QY      265 sLeuLysGlyHisLeuAsnGlySerValAlaAlaValAsnGlyHisThrAsnSerPhePro 285
Db      367 CCTCAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 426
QY      285 sSerLeuGluAspSerValLysProArgLysGlnAlaLysAsp 299
Db      427 ACTGCTGGAAATCAATGTGTGAAGGCAAGGAAGTGTGGGAAAGAT 469

RESULT 9
US-09-918-995-37438
: Sequence 37438, Application US/09/918995
: Publication No. US2003007462A1
: GENERAL INFORMATION:
: APPLICANT: Hyseq, Inc.
: TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
: FILE REFERENCE: 20411-756
: CURRENT APPLICATION NUMBER: US/09/918,995
: CURRENT FILING DATE: 2001-07-40
: PRIOR APPLICATION NUMBER: US/09/245,076
: PRIOR FILING DATE: 1999-01-20
: NUMBER OF SEQ ID NOS: 38054
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 37438
: LENGTH: 384
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)...(484)
: OTHER INFORMATION: n = A,T,C or G
US-09-918-995-37438

Alignment Scores:
Pred. No.: 1,196-54 Length: 484
Score: 548.00 Matches: 99
Percent Similarity: 97.20% Conservative: 5
Best Local Similarity: 92.52% Mismatches: 3
Query Match: 33.19% Indels: 0
Db: 9 Gaps: 0

US-09-624-670-64 (1-299) x US-09-918-995-37438 (1-484)
QY      1 MetGluHisPheAspAlaSerLeuSerThrTyrPheLysAlaPheLeuGlyProArgAsp 20
Db      62 ATGGAACATTTTCATGTCATGACATAGTACCTATTTCAAGCAATGCTAGCTGCTGCTGCTGCTGCT 121
QY      21 ThrArgValLysLysTyrPhePheLeuLeuAspAspTyrIleProGlnHisValLysSerVal 40
Db      122 ACTAGACTAAAGGAGGCTTTCTCTCTGGACCAATATATAATCAATATATGCTGCTGCTGCTGCTGCT 181
QY      41 PheTyrLeuLeuLeuValTrpLeuGlyProArgSerPheMetLysAsnArgGlnLeuProPheSer 60
Db      182 ATATATTTTACTAATTTGATGCTGGGACCAATATATATGGAATATATATATATATATATATATATAT 241
QY      61 CysArgGlyIleLeuLeuLeuLeuTyrAsnLeuGlyLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 80
Db      242 TGGCGGGGGGATTTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 301
QY      81 TyrGlnLeuValThrGlyValIleProLeuLysTyrAsnPheProCysGlyThrArg 100
Db      302 TGTCAATTACTAAGCAGGACTATGGGAAGGCAATATCAATATATATATATATATATATATATATATAT 361

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GenCore version 5.1.6
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CM protein nucleic search, using frame_plus_p2n model

Run on June 15, 2003, 21:36:46; Search time: 1190.54 seconds
(without alignments)
4066 072 Million cell updates/sec

Title: US-09-624-670-64

Perfect score: 1651

Sequence: 1 MHHFPAASLSTYFKAFICPPQ HTNSFPSI PMSVPRKPKPKD 299

Scoring table:

BLOSUM62 Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Zgapop 6.0, Zgapext 7.0
Delop 6.0, Deloxt 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-G=us09-624-670-64 -L=us09-624-670-64 -F=us09-624-670-64 -M=us09-624-670-64
-DB=EST -QFMT=fastap -SUBFMT=fast -MINMATCH=0.1 -LCL=us09-624-670-64 -LCLFMT=0
-UNITS=bits -START=1 -ENDS=1 -MATRIX=BLOSUM62 -TRANS=human40.cdi -LIST=45
-LOCAL=200 -THRESHOLD=100 -THRESHOLD=100 -THRESHOLD=100 -THRESHOLD=100
-OUTFMT=ps -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=us09624670 -GNN_1_1_374 -FPMAT=11062003_075430_11642 -ICPU=3
-NO_MMAB -LARGEQUERY -NLS -SUFFS=0 -WAIT -DISPBL="K=100 -L=us09-624-670-64
-DEF_TIMEOUT=120 -WARN_TIMEOUT=30 -THRESHOLD=1 -XGAPOP=10 -XGAPEXT=0.5 -FCGAPOP=6
-FCGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DEFEXT=7

Database :

EST: *
1: em_estba: *
2: em_esthum: *
3: em_estlin: *
4: em_estmu: *
5: em_estov: *
6: em_estpl: *
7: em_estro: *
8: em_hic: *
9: gb_est1: *
10: gb_est2: *
11: gb_hic: *
12: gb_est3: *
13: gb_est4: *
14: gb_est5: *
15: em_estfun: *
16: em_estom: *
17: gb_gss: *
18: em_gss_hum: *
19: em_gss_inv: *
20: em_gss_pla: *
21: em_gss_vrt: *
22: em_gss_fun: *
23: em_gss_hum: *
24: em_gss_mus: *
25: em_gss_ofber: *
26: em_gss_pro: *
27: em_gss_rud: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1530	92.7	941	9	AL559414	AL559414 AL559414
2	1402	84.9	900	13	BI693107	BI693107 603344472
3	1351.5	81.9	950	9	AL553407	AL553407 AL553407
4	1337	80.4	897	14	H0884263	H0884263 AGENCOURT
5	1309	79.3	861	9	AL514872	AL514872 AL514872
6	1300	78.7	843	14	H0217076	H0217076 AGENCOURT
7	1290.5	78.2	991	14	H0895704	H0895704 AGENCOURT
8	1219	73.8	785	9	H0079897	H0079897 A0079897
9	1217.5	73.7	700	13	H1155440	H1155440 602903816
10	1178	71.4	902	9	AL516234	AL516234 AL516234
11	1164.5	70.5	932	9	AL552819	AL552819 AL552819
12	1164	70.5	961	14	H0936171	H0936171 AGENCOURT
13	1158	70.1	375	13	R1853179	R1853179 603379527
14	1152	59.8	397	14	H0213770	H0213770 AGENCOURT
15	1140	59.0	561	10	H0080106	H0080106 RC4-BT062
16	1132	58.0	796	10	H0535118	H0535118 601231235
17	1119	67.8	760	9	AL548756	AL548756 AL548756
18	1119	67.4	884	13	BI597218	BI597218 603256086
19	1113.5	67.4	884	13	BI597218	BI597218 603256086
20	1113	67.4	884	13	BI597218	BI597218 603256086
21	1112.5	67.4	862	13	H1835075	H1835075 603087730
22	1091	66.1	927	12	H0213449	H0213449 602363905
23	1053	63.8	748	12	H0270622	H0270622 188609.7
24	1047	63.4	712	13	BI327811	BI327811 602979561
25	1046	63.4	716	14	BI328570	BI328570 602985371
26	1042.5	63.1	712	14	H0971432	H0971432 602843085
27	1042	63.0	582	12	H0971432	H0971432 602843085
28	1032.5	62.5	907	12	H0100925	H0100925 601753670
29	1032	62.5	810	12	H0251449	H0251449 602363905
30	997.5	60.4	800	13	BI568778	BI568778 603294725
31	995	60.3	735	9	AL518949	AL518949 AL518949
32	990	60.0	666	10	BB659205	BB659205 BB659205
33	987	59.8	694	14	BM788585	BM788585 K-EST0067
34	970	58.8	635	10	H0615265	H0615265 BB615265
35	956.5	57.9	800	11	AK014803	AK014803 Mus muscu
36	952	57.7	627	10	BB613066	BB613066 BB613066
37	927	56.1	1150	13	BM461375	BM461375 AGENCOURT
38	925.5	56.1	969	12	BF161512	BF161512 601771006
39	923	55.9	712	13	H0523961	H0523961 HJ523961
40	897	54.3	694	12	H0741563	H0741563 602695171
41	887	53.7	620	10	BB657364	BB657364 BB657364
42	885	53.6	677	10	BB643510	BB643510 BB643510
43	881	53.4	614	10	BB661704	BB661704 BB661704
44	877.5	53.1	749	13	BI463309	BI463309 603204321
45	870	52.7	1028	14	H0895633	H0895633 AGENCOURT

ALIGNMENTS

RESULT 1
AL559414
LOCUS
DEFINITION AL553414 L11_NFL008_T02 Homo sapiens cDNA clone CS0DJ013VD07 5
prime, mRNA sequence.
ACCESSION AL559414
VERSION AL559414.1 GI:12904892
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 941)
AUTHORS Li, W.-H., Gruber, C., Li, S.-S., Li, J. and colleagues, H.
TITLE Full-length cDNA libraries and normalization

JOURNAL
COMMENT

Unpublished (2001)
Contact: Genoscope
Centre National de Sequencage
BP 191 91006 EVRY cedex France
Email: seq@genoscope.cns.fr, Web : www.genoscope.cns.fr
Location/Qualifiers
1. 941
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS001013YD07"
/clone_lib="HL1_NF1008_PC2"
/sex="male"
/issue_type="T cells from T cell leukemia"
/note="Vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

FEATURES
source

BASE COUNT 242 a 242 c 204 g 262 t others
ORIGIN

Alignment Scores:

Pred. No.: 8,240,168 Length: 941
Score: 1540,00 Matches: 277
Percent Similarity: 96.99% Conservatives: 13
Best Local Similarity: 92.64% Mismatches: 9
Query Match: 92.67% Indels: 1
Gaps: 0

US-09_624_670_64 (1-299) x AL559414 (1-941)

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DB 33 ATGCAATTTTATGACGACACTAGTACCTATTTCAAGGCATTCGACCCCTCCAGAT 92
QY 21 ThrArqValLysGlyTyrPheLeuLeuAspAspAspTyrTleProThrPheValCysSerVal 40
DB 93 ACTAGAGTAAAGGATGTTCTCTCGGACAAATATATACCCACATTTATCTGCTGTC 152
QY 41 TleTyrLeuLeuLeuValTyrPheLeuGlyProLysTyrMetLysAsnArqGlnProPheSer 63
DB 153 ATATATTACTAAATGATAGCTGTGGACAAAATACATGACGAATAAAGACGACATCTCT 212
QY 61 CysArqGlyTleLeuLeuLeuTyrAsnLeuGlyLeuThrLeuLeuSerLeuTyrMetPhe 80
DB 213 TGGCGGGGATTTATGCTGTATACCTTGGACATCACACTCTCTCTCTCTATATGCTC 272
QY 81 TyrGluLeuValThrGlyValTyrGlyGlyLysTyrAsnPhePheCysGlnGlyThrArq 100
DB 273 TGTAGTTAGTAAAGAGATATGGAAGAAATAAATATTTCTGTCAAGGACAAAGC 332
QY 101 SerAlaGlyCysSerAspMetLysTleLeuArqValLeuTyrTyrTyrPheSerLys 120
DB 333 ACCGACAGCAATACATATGACATATCCGTCCTCTGTCGGTACTACTTCGCCAA 391
QY 121 LeuLeuGluPheMetAspThrPhePhePheLeuLeuArqLysAsnAsnIleThr 140
DB 392 CTCATACATTTTAGGACATTTCTCTCTCTCATCCGCGCAAGCAACACCCAGATCAG 451
QY 141 ValLeuHisValLysHisHisAlaThrMetLeuAsnIleTyrTyrPheValMetAsnTrp 160
DB 452 GTCCGACGCTACACACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 511
QY 161 ValProCysGlyHisSerTyrPheGlyAlaThrLeuAsnSerPheLeuHisValLeuMet 180
DB 512 GTCCCCGCGGACACTCTATTTTGTGGCACACTTAATAGCTTCATCCACCTCCCTCAG 571
QY 181 TyrSerTyrTyrGlyLeuSerSerLeuProSerMetArqProTyrLeuTyrTrpLysLys 200

DB 572 TATCTTACTATGATGTTGTCAGAGCTTCTATGATGATGATGATGATGATGATGATGATG 631
QY 201 TyrTleThrGlnGlyLeuValGlnPheValLeuThrTleTleGlnThrThrCysSly 220
DB 632 TATATATCTAGAGGGAAGTGTATTCAGTTTGATGATGATGATGATGATGATGATGATG 691
QY 221 ValPheTrpProCysSerPhePhePheLeuGlyTyrPheLeuThrPheLeuThrTyrMetTle 240
DB 692 GTATCTGGCGGTGCATATCCCTCTGGTGTGTGTATTCAGATTCAGATTCAGATTCAG 751
QY 241 SerLeuIleAlaLeuPheThrAsnPheTyrTleGlnThrTyrAsnLysSlyAlaSer 260
DB 752 TCCGTATGTTGTCGTTCACAACTTCTCAATTCATCAATCAATCAATCAATCAATCAAT 811
QY 261 ArgArqLysAspHisLeuLysGlyHisGlnAsnGlySerValAlaAlaValAsnGlyHis 280
DB 812 CGAAGAAAGAACACCTGAGAGAACACCAATAGGTGTCATGTGTGTGTAATGACAC 871
QY 281 ThrAssSerPheProSerLeuGluAsnSerValLysProArqLysGlnArqLysAsp 299
DB 872 ACCAACACCTTTTCACCTCCCGGAAACAAATGACAGCAAGCAAGCAAGCAAGCAAG 928

RESULT 2

BF693107

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

NIH-MDC http://mrc.ncl.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: rquabb@mail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: The T.M.A.G.E. Consortium (LLNL)

Clone distribution: MGC clone distribution information can be

found through the T.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: L1AM11947 row 10 column 18

High quality sequence stop: 797

Location/Qualifiers

1. 900

/organism="Mus musculus"

/strain="FVB/N-4"

/db_xref="taxon:10090"

/clone="IMAGE:5472493"

/clone_lib="N1_CGAP_Mam2"

/issue_type="tumor, biopsy sample"

/dev_stage="5 months"

/lab_host="D10H"

/note="Organ: mammary; Vector: pCMV SPORT6; Site 1: SalI;

Site 2: NotI; Cloned unidirectionally. Primers: oligo dT;

Library constructed by Life Technologies. Investigator

providing samples: Gilbert Smith, NIH"

BASE COUNT 208 a 258 c 198 g 246 t

ORIGIN

Alignment Scores:

Pred. No.: 6,690,153 Length: 900

Score: 1402,00 Matches: 263

Percent Similarity: 93.45% Conservatives: 16

Best Local Similarity: 90.69% Mismatches: 15

Query Match: 84.92% Indels: 4

QY 161 ValProCysGlyHisSerTyrPheGlyAlaThrLeuAsnSerPheIleHisValLeuMet 180
 DB 602 GTCCCTGGGAGACTTATTGGTGGACACTTAATATAGCTTCATGACAGGCTCATG 561
 QY 181 TyrSerTyrTyrGlyLeuSerSerIleProSerMetAlaProTyrLeuTyrTrpLysLys 200
 DB 662 TACTGTATATAGGTGTGTGTCAGTCCCTCCATGCTCCATACCTTCGTGGAGAAAG 721

QY 201 TyrIleThrIleGlnGlnValGlnPheValLeuThrIleIleGlnThrThrCysGly 220
 DB 742 TATATCATGATGAGGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 781
 QY 221 ValPheThrProCysProPheGlnGlnTyrPheGlnPheGlnGlnTyrMetIle 240
 DB 782 GTCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840

QY 241 SerLeuIleAlaLeuPheThrAsnPheTyrIleGlnThrTyrAsnLysLysGlyAlaSer 260
 DB 841 TCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
 QY 261 ArgArgLysAspHisIleValGlyGlyHisAsnSerTyr 273
 DB 900 GGAAGGAAAGACACT GAAGACACAGAAATGGTCA 936

RESULT 4
 HQ883263
 LOCUS
 DEFINITION AGNCOURT_8727526 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:6340766
 5' mRNA sequence.

ACCESSION HQ883263
 VERSION HQ883263.1 GI:22275271
 KEYWORDS EST.

SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 897)
 AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>
 TITLE National Institutes of Health Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cdapub@mail.nih.gov
 Tissue procurement: ATCC
 cDNA library preparation: Rubin Laboratory
 cDNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: t4CM2537 row: 1 column: 15
 High quality sequence stop: 688.

FEATURES
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 /note="organ: brain; Vector: pORI7; site_1: XhoI; site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into pORI/XhoI sites using the following 5' adapter: 32ACGAG(G). Size-selected 550bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC library."
 BASE COUNT 211 a 245 c 194 g 257 t
 ORIGIN

Alignment Scores:

Pred. No.:

4,76c144

Length:

897

Score: 1427.00 Matches: 245
 Percent Similarity: 95.90% Conservations: 12
 Best Local Similarity: 91.42% Mismatches: 4
 Query Match: 80.48% Indels: 0
 DB: 14 Gaps: 0

us-09-624-670-64 (1 299) x 0.2983263 (1 897)

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QY 21 ThrArgValLysGlyThrPheLeuAspAsnTyrIleProPhePheValCysSerVal 40
 DB 150 ATATAGTAT 209

QY 41 IleTyrLeuLeuIleValTyrLeuGlyThrGlyTyrMetLysAsnArgGlnProPheSer 60
 DB 210 AT 269

QY 61 CysArgGlyIleLeuGlnLeuTyrAspLeuGlyLeuThrLeuLeuSerLeuTyrMetPhe 80
 DB 270 TGGCGGGGGATTTTATGGGCTATACCTTGGATTCATACCTTGGCTTGTATATATGTC 429

QY 81 TyrGlnValThrGlyValTyrPheGlyLysTyrAsnThrPheCysGlnGlyThrArg 100
 DB 340 TGTGATTTAGTAAACAGGATGATGGAGGAAATATAATATATATATATATATATATAT 489

QY 101 SerAlaGlyGlnSerAspMetLysIleIleValValLeuThrTrpTyrTyrPheSerLys 120
 DB 390 ATGACAGACAAATACAAATGAAATATATATATATATATATATATATATATATATAT 449

QY 121 LeuIleGluPheMetAspThrPhePheIleLeuAlaGlyAsnAsnIleIleThr 140
 DB 450 CTATATAAATTTATGGACACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 509

QY 141 ValLeuHisValTyrHisHisAlaThrMetLeuAsnIleTrpTrpPheValMetAsnTrp 160
 DB 510 GTCTGAGAGTAT 569

QY 161 ValProCysGlyHisSerTyrPheGlyAlaThrLeuAsnSerPheIleHisValLeuMet 180
 DB 570 GTGCGCGCGGCGGACACTTATTTGGTGGACACTTAAATATATATATATATATATAT 629

QY 181 TyrSerTyrTyrGlyLeuSerSerIleProSerMetAlaProTyrLeuTrpTrpLysLys 200
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QY 201 TyrIleThrGlnGlyGlnValGlnPheValIleThrIleIleThrThrThrCysGly 220
 DB 690 TAT 749

QY 221 ValPheTrpProCysSerPheProLeuGlyTyrPhePhePheIleGlyTyrMetIle 240
 DB 750 GTCAATGCGCGGCGGACACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 809

QY 241 SerLeuIleAlaLeuPheThrAsnSerTyrIleGlnThrTyrAsnLysLysGlyAl 269
 DB 810 TTCTCTGATGCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 869

QY 259 AsnArgAlaLysAsp 264
 DB 870 TTGCGGAGAGAGAGAA 885

RESULT 5
 HQ883263
 LOCUS
 DEFINITION AL514872 L11 NP1006 P12 Homo sapiens cDNA clone cl0080142P12 5
 Patient: alpha sequence.
 ACCESSION AL514872
 VERSION AL514872.1 GI:12778465
 KEYWORDS EST.
 SOURCE human.

AL514872 861 bp mRNA linear EST 14 FEB-2001
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 861)
AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, web: www.genoscope.cns.fr
FEATURES
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was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies, contain: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com"
BASE COUNT 193 a 232 c 180 g 256 t
ORIGIN
Alignment Scores:
Pred. No.: 4,49e-142 Length: 861
Score: 1309.00 Matches: 235
Percent Similarity: 98.01% Conservative: 11
Best Local Similarity: 93.64% Mismatches: 5
Query Match: 79.29% Indels: 1
DB: Gaps: 0
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QY 1 MetGluHisPheAspAlaSerLeuSerThrTyPheLysAlaPheLeuGlyProArgAsp 20
Db 108 ATGACACATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 167
QY 21 ThrArgValLysGlyTrpPheLeuLeuAspAsnTrpLeuProThrPheValCysSerVal 40
Db 168 ACTAGAGTAAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 227
QY 41 IleTyPheLeuLeuValTrpLeuGlyProLysTyPheMetLysAsnArgGlnProPheSer 60
Db 228 ATATATTACTAATTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 287
QY 61 CysArgGlyIleLeuGlnLeuTyPheAsnLeuGlyLeuThrLeuLeuSerLeuTyPheMetPhe 80
Db 288 TGGGGGGGATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 347
QY 81 TyPheLeuValThrGlyValTrpGluGlyLysTyPheAsnPhePheCysGlnGlyThrArg 100
Db 348 TGTGAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 407
QY 101 SerAlaGlyCysSerAspMetLysIleIleArgValLeuTrpTrpTyPheSerLys 120
Db 408 ACTGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 465
QY 121 LeuIleGluPheMetAspThrPhePhePheIleLeuArgLysAsnAsnHisGlnIleThr 140
Db 467 CTCAGAGATTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 526
QY 141 ValLeuHisValTyPheHisAlaThrMetLeuAsnIleTrpTrpPheValMetAsnTrp 160
Db 527 GTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 586
161 ValProCysGlyHisSerTyPheGlyAlaThrLeuAsnSerPheIleHisValLeuMet 180
Db 587 GTCCTGCGGGGATCTCTATTTTGGTGGACACTTAATAGCTTCATCCACGCTCCTCATG 646
QY 181 TyPheTrpTyPheGlyLeuSerSerIleProSerMetArgProTyPheLeuTrpTrpLys 200
Db 647 TACTTTTACTATGTTTGGTGGACGCTTCCTCATGCTGCTGCTGCTGCTGCTGCTGCTG 706
QY 201 TyPheTrpGlnGlyLeuValGlnPheValLeuThrIleGlnThrThrCysGly 220
Db 707 TACATCATCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 766
QY 221 ValPheTrpProCysSerPheProLeuGlyTrpLeuPhePheGlnIleGlyTyPheIle 240
Db 767 GTCACTGCGGCTGGTGGACATTCCTTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 826
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ACCESSION BQ217076
VERSION BQ217076.1
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SOURCE human.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 893)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: rqb@bbsr@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLNL3291 row: 3 column: 22
High quality sequence stop: 716.
FEATURES
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Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
BASE COUNT 194 a 245 c 193 g 261 t
ORIGIN
Alignment Scores:
Pred. No.: 5,28e-141 Length: 893
Score: 1300.00 Matches: 231
Percent Similarity: 97.59% Conservative: 12
Best Local Similarity: 92.77% Mismatches: 5
Query Match: 78.74% Indels: 1
DB: Gaps: 0
US-09-624-670-64 (1-299) x BQ217076 (1-893)

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 DB 147 ATGGAAATATTTGATGATCATCTAGTACTAGTATTTCAAGGATGTTGATGAGCTAGAT 206
 QY 21 ThrArgValLysGlyTyrPheLeuLeuAsnTyrIlePheThrPheValCysSerVal 40
 DB 207 ACTACAGTAAAGCAATGCTTCTCTGCAAAATATATATATCCACATTTATCTGCTGTC 266
 QY 41 IleTyrLeuLeuIleValTyrLeuGlyProLysTyrMetLysAsnArgLysProPheSer 60
 DB 267 ATATATTTATTAATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 326
 QY 61 CysArgGlyIleLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 80
 DB 427 TGGGAGGATTTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 386
 QY 81 TyrGluLeuValThrGlyValTyrPheLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 100
 DB 487 TGTGAGTTAGTAAATAGAGTATGGAAGGCAATATAGAACTTCTCTGCTGCTGCTGCT 446
 QY 101 SerAlaGlyIleLeuSerAspMetLysIleIleValValLeuTyrPheTyrPheSerLys 120
 DB 447 ACCGACGAGCAATAGATATAGATATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 506
 QY 121 LeuIleGluPheMetAspThrPhePhePheIleLeuArgLysAsnHisGlnIleThr 140
 DB 507 CTCATAGAAATTTATGAGATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 566
 QY 141 ValLeuHisValTyrHisHisAlaThrMetLeuAsnIleTyrPheValMetAsnTrp 160
 DB 567 GTCTGTCACGCTACCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 626
 QY 161 ValProCysGlyHisSerTyrPheGlyAlaThrLeuAsnSerPheIleHisValLeuMet 180
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 QY 181 TyrSerTyrTyrTyrLeuSerSerLeuPheSerMetArgPheTyrLeuTyrPheLys 200
 DB 687 TACTTCTATGATGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 746
 QY 201 TyrIleThrIleGlyIleValGlnPheValLeuThrIleIleGlnThrThrCysGly 220
 DB 747 TACATCATCAGGCGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 806
 QY 221 ValPheTrpPheCysSerPheProLeuGlyTyrPhePhePheGlnIleGlyTyrMet 240
 DB 807 GTCATCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 866
 QY 240 eSerLeuIleAlaLeuPheThrAsn 248
 DB 867 TTCTCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 891

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 H0895704
 VERSION B0895704.1 GI:224287718
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Chordata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 991)
 NIH-MG http://mg. nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: ecapbs@mail.nih.gov
 Tissue Procurement: Mark Macdonald, Ph.D. and Nancy L. Freeman, Ph.D.
 cDNA Library Preparation: RosGen, Invitrogen Corp

cDNA Library Arrayed by: the I.M.A.G.E. Consortium (LIML)
 DNA Sequencing by: Amersham Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at:
 http://image.llnl.gov
 Plate: L1AM13784 row: n column: 11
 High quality sequence stop: 660.
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 BASE COUNT 213 a 229 g 260 t
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 Pred. No.: 7,74e-140 Length: 991
 Score: 1290.50 Matches: 254
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 Best Local Similarity: 86.99% Mismatches: 18
 Query Match: 78.16% Indels: 13
 DB: 14 Gaps: 4
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 QY 1 MetGluHisPheAspAlaSerLeuSerThrTyrPheLysAlaPheLeuGlyProArgAsp 20
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 QY 21 ThrArgValLysGlyTyrPheLeuLeuAsnTyrIlePheThrPheValCysSerVal 40
 DB 180 ACAAGATCAAAAGATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 249
 QY 41 IleTyrLeuLeuIleValTyrLeuGlyProLysTyrMetLysAsnArgLysProPheSer 60
 DB 240 ATTTACTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTAT 299
 QY 61 CysArgGlyIleLeuSerAspMetLysIleIleValValLeuThrIleIleGlnThrThr 80
 DB 366 TGGGAGGATTTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 459
 QY 81 TyrGluLeuValThrGlyValTyrPhePhePheGlnIleGlyTyrMet 100
 DB 360 TATGATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 419
 QY 101 SerAlaGlyIleLeuSerAspMetLysIleIleValValLeuThrIleIleGlnThrThr 120
 DB 420 AGCGCGAGCAATCCCATATGAGATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 479
 QY 121 LeuIleGluPheMetAspThrPhePhePheIleLeuArgLysAsnHisGlnIleThr 140
 DB 486 CTCATCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 549
 QY 141 ValLeuHisValTyrHisHisAlaThrMetLeuAsnIleTyrPheValMetAsnTrp 160
 DB 549 GTCTGTCACGCTACCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 599
 QY 161 ValProCysGlyHisSerTyrPheGlyAlaThrLeuAsnSerPheIleHisValLeuMet 180
 DB 600 GTCTGTCACGCTACCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 659
 QY 181 TyrSerTyrTyrLeuSerSerLeuPheSerMetArgPheTyrLeuTyrPheLys 200
 DB 660 TACTTCTATGATGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 719
 QY 201 TyrIleThrIleGlyIleValGlnPheValLeuThrIleIleGlnThrThrCysGly 220


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BQ936171
LOCUS      961 bp      mRNA      Linear      EST 21-AUG-2002
DEFINITION AGENCOURT-B857100 NCI_CGAP_Mam2 Mus musculus cDNA clone
IMAGE:6441266.5, mRNA sequence.
ACCESSION  BQ936171
VERSION     BQ936171.1  GI:22451554
KEYWORDS   EST.
SOURCE     house mouse.
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sclerogomathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 961)
            NIH-MC-171-151 sub. 1.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: eap@rsbmail.nih.gov
            Tissue Procurement: Gilbert Smith, Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Amersham Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLM1964 row: d column: 04
            High quality sequence stop: 530.
            Location/Qualifiers
                location: 1..961
                organism: "Mus musculus"
                strain: "FVB/N-3"
                db_xref: "taxon:10090"
                /clone: "IMAGE:6441266"
                /clone_lib: "NCI_CGAP_Mam2"
                /tissue type: "tumor, biopsy sample"
                /dev stage: "5 months"
                /lab host: "DH10B"
                /note: "Organ: mammary; Vector: pCMV-Sport6; Site 1: SalI;
                Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
                Library constructed by Life Technologies. Investigator
                providing samples: Gilbert Smith, NIH"
BASE COUNT  212 a 279 c 242 g 238 t
ORIGIN
Alignment Scores:
  Prod. No.: 4,286,125 Length: 961
  Score: 1167.00 Matches: 232
  Percent Similarity: 94.72% Conservatve: 1
  Best Local Similarity: 94.41% Mismatches: 6
  Query Match: 70.50% Indels: 8
  DB: 14 Gaps: 0
US-09-624-670-64 (1-299) x BQ936171 (1-961)
QY 60 SerCysArgGlyTyrPheGlyValThrLeuAspSerPheThrHisValLeu 79
Db 1 TCTTCGAGGACATCGTGAATTGAT-AACTTGACTACCGCTGCTCTACATG 59
QY 80 PheTyrGlnLeuValThrGlyValThrPhePhePhePheCysGlnGlyThr 99
Db 60 TCTATGAGTGTGATGCAACAGTGTGTGGAAAGGCAATATGATGCTTTTTCGAGGAA 119
QY 100 ArgSerAlaGlyLeuSerAspMetLeuGlyLeuValLeuThrPheTyrPheSer 119
Db 120 CGCAGCGCGGAGAAACCGCAATGACAGATGATACGCGCTCTCTCGGGGACACTTCCT 179
QY 120 LysLeuLeuThrLeuMetAspThrPhePhePhePhePhePhePhePhePhePhe 139
Db 180 AAATCATCGAATTCATGAGAACCTTTTCTTCATCTTCGCAAAACAAACCCAGATC 249
QY 140 ThrValLeuHisValThrHisHisAlaThrMetLeuAsnLeuThrPheValMetAsn 159
Db 240 ACCGTGTCATGTCATGACACAGCTAGCATGCTTAAATCTGCTGCTTTGTGATGAC 299
160 TrpValProCysGlyHisSerTyrPheGlyValThrLeuAspSerPheThrHisValLeu 179
Db 300 TGGTTCCTTCGGGCAATTCATATTTTGGTGACATCAAAAGTTCATCAATCAATGCTTC 259
QY 180 MetTyrSerTyrTyrGlyLeuSerSerLeuProSerMetAspThrPheLeuThrPhePhe 199
Db 360 ATGTACTGTACTATGGGTGCTGCTCATACAGGTCATGAGGAGGAGGCTACTCTGTGTG 419
QY 290 LysTyrThrThrGlnGlyGlnLeuValLeuThrPheValLeuThrPheLeuThrPhe 219
Db 420 AAGTACATCACTCAAGGCGACGTCGCTCCAGTTCTGTGACAAATCAATCAATCAATGCT 479
QY 220 GlyValPheThrPhePhePhePhePhePhePhePhePhePheGlnGlyTyrMet 239
Db 480 GGGGCTTCGGGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 539
QY 234 ThrSerGlnLeuValLeuThrPheThrAspPheTyrThrGlnThrThrPheAspLys 258
Db 540 GATTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 599
QY 259 AlaSerArg-ArgLysAspHisLeuLysGlyHisHisGlnAsnGlySerValAlaAlaValAs 278
Db 600 GGCCTCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 659
QY 278 GlnGlyHisThrAspSerPheProSerLeuGlyAlaAsnSerValLysProArgLysGlnArg 297
Db 660 GGCACATCAACCAACAAAGCTTCCTTCGCAAAACAGCTGCAAAACAGCTGCAAAACAG 719
QY 297 GlnSer 298
Db 720 GAAA 724
RESIDUE 13
BQ936179
LOCUS      875 bp      mRNA      Linear      EST 10-OCT-2001
DEFINITION 603375527E1 NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5489606.5,
            mRNA sequence.
ACCESSION  BQ936179
VERSION     BQ936179.1  GI:15993926
KEYWORDS   EST.
SOURCE     house mouse.
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sclerogomathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 875)
            NIH-MC-171-151 sub. 2.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: eap@rsbmail.nih.gov
            Tissue Procurement: Lothar Hennighausen Ph.D., Ph.D. Xie Dong Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Lucyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLM11993 row: c column: 07
            High quality sequence stop: 792.
            Location/Qualifiers
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                /accession: "Mus musculus"
                /strain: "FVB/N-EV/N"
                /db_xref: "taxon:10090"
                /clone: "IMAGE:5489606"
                /clone_lib: "NCI_CGAP_Mam3"
                /tissue type: "tumor, gross tissue"
                /dev stage: "10 months"
                /lab host: "DH10B"
                /note: "Organ: mammary; Vector: pCMV-Sport6; Site 1: SalI;
                Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
                Library constructed by Life Technologies. Investigators
                providing samples: Lothar Hennighausen/Ph.D. Xie Dong, NIH

```

Reference for transgenic model: Xu et al., Nature Genetics
22: 37-43 (1999).

BASE COUNT 188 a 256 c 191 g 240 t

ORIGIN

Alignment Scores:

Pred. No.: 1 90-124 Length: 875
Score: 1158.00 Matches: 244
Percent Similarity: 92.57% Conservativity: 5
Best Local Similarity: 90.71% Mismatches: 14
Query Match: 70.14% Indels: 12
DB: 13 Gaps: 0

US-09-624-670-64 (1-299) x H1853179 (1-875)

Qy 1 MetGluHisPheAspAlaSerLeuSerThrTyrPheLys--AlaPheLeuLeuValProArgA 20
Db 85 ATGGAACATTTTCATTCCTCAGTACCTATTTCGAATGGCTTCCTGGGCCCGAG 144
Qy 20 sPThrArgValLysGlyTrpPheLeuLeuAspAsnTyrIleProThrPheValCys-Ser 39
Db 145 ATACAGAGTCAGAGGATGGTCTCTCTGGACATTACATCCCTACGTTTGCTGTCTCT 204
Qy 40 Val-IleTyrLeuLeu-IleValTrpLeuGlyProLysTyrMetLysAsnArgGlnProp 59
Db 205 GTTACGTTTACCTACATCTGATGCTGGGACCAAAATACATCAAGACCGGCGGT 264
Qy 59 heSerCysArgGlyIleLeuGlnLeuTyrAsnLeuGlyLeuThrLeuLeuSerLeuTyrM 79
Db 265 TCTCTTGGGAGGCAATCTGGAGTTGTATACCTTGGACACACCTCTCTCTCTCTCA 324
Qy 79 ethcTyrGluLeuValThrGlyValTrpGlyLysTyrAsnPhePheCysGlnGlyT 99
Db 325 TCTTTATGATGTTGTAAGCTGTCTGTAAGGAAAFANATTTTCTGGTGGAGGAA 384
Qy 99 hrArgSerAlaGlyGluSerAspMetLysIleIleArgValLeuTrpTrpTyrTyrPheS 119
Db 385 CACGCGACCGGAGCAATCCGATAGAAGATCATCCCGGTCTCTCTGCTACTCTCT 444
Qy 119 erLysLeuIleGluPheMetAspThrPhePhePheIleLeuArgLysAsnLysGlnI 139
Db 445 CCAAACTCAAGAAATCATGACACATCTTTCTCTATCTCTCTCTCTCTCTCTCT 504
Qy 139 leThrValLeuHisValTyrHisHisAlaThrMetLeuAsnIleTrpTrpPheValMetA 159
Db 505 TCAAGCTGATCAAGTCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 564
Qy 159 snTrpValProCysGlyHisSerTyrPheGlyAlaThrLeuAsnSerPheIleHisValI 179
Db 565 ACTGGCTTCT 624
Qy 179 euMetTyrSerTyrTyrGlyLeuSerSerIleProSerMetArgProTyrLeuTrpTrpL 199
Db 625 TCAAGTACTGAAATCAAGGATGATGATGATGATGATGATGATGATGATGATGAT 684
Qy 199 yLys-TyrIleThrGlnGlyGlnLeuValGlnPheValLeuThrIleGlnThrThr 218
Db 685 AAAATTTTATCAATCAAGGATGATGATGATGATGATGATGATGATGATGATGAT 743
Qy 219 CysGlyValPheTrpProCysSerPheProLeuGlyTrpLeuPhePheGlnIleGlyTyr 238
Db 744 TCGGCT 798
Qy 239 MetIleSerLeuIleAlaLeuPheThrAsnPheTyrIleGlnThrTyrAsnLysLysGly 258
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Qy 259 AlaSerArgArgLys 263
Db 859 CT-TCTCGAGAAAAA 872

RESULT 14
HQ213770

LOCUS
DEFINITION

BQ213770 897 bp mRNA linear EST 02-MAY-2002
AGENCOUNT_708012 NIH_MCC_72 Homo sapiens cDNA clone IMAGE:6064578
5', mRNA sequence.

ACCESSION BQ213770

VERSION BQ213770.1 GI:20395170

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Homnidae, Homo.
REFERENCE 1 (bases 1 to 897)
NIH-MGC <http://mgc.nci.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
CONTACT: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC/DCID/DTP
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lln.gov>

AUTHORS

TITLE

JOURNAL

COMMENT

Plate: L1AM1339 row: h column: 19
High quality sequence stop: 625.
Location/Qualifiers
1. .897
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/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ skin, Vector pCMV SPORT6, Site_1: NotI,
Site_2: SalI, Cloned unidirectionally. Primer, Oligo dt.
Average insert size 2 kb. Library constructed by Life
Technologies."

FEATURES

source

BASE COUNT 212 a 233 c 198 g 253 t 1 others

ORIGIN

Alignment Scores:

Pred. No.: 9 85e-124 Length: 397
Score: 1152.00 Matches: 213
Percent Similarity: 94.12% Conservativity: 11
Best Local Similarity: 89.50% Mismatches: 9
Query Match: 69.78% Indels: 5
DB: 14 Gaps: 1

US-09-624-670-64 (1-299) x BQ213770 (1-897)

Qy 1 MetGluHisPheAspAlaSerLeuSerThrTyrPheLysAlaPheLeuGlyProArgAsp 20

Db 84 ATGGAACATTTTCATTCCTCAGTACCTATTTCGAATGGCTTCCTGGGCCCGAGAT 143

Qy 21 ThrArgValLysGlyTrpPheLeuLeuAspAsnTyrIleProThrPheValCysSerVal 40

Db 144 ACTAGAGTAAAGAAAGAGGTTTCTTCTTGAATAATTATATA CCAATTATTCTCTGTGC 203

Qy 41 IleTyrLeuLeuIleValTrpLeuGlyProLysTyrMetLysAsnArgGlnProPheSer 60

Db 204 ATATATTTACTAATTTGTATGGCTGGACCAAAATACATGAGGAATAAACAGCCATTCTCT 263

Qy 61 CysArgGlyIleLeuGlnLeuTyrAsnLeuGlyLeuThrLeuLeuSerLeuTyrMetPhe 80

Db 264 TGGCGGAGGATTTTATTTGTTGTTATTAATCTTGAATCTTGAATCTTGAATCTTGA 323

Qy 81 Ty-GluLeuValThrGlyValTrpGluGlyLysTyrAsnPhePheCysGlnGlyThrArg 100

Db 324 TGTGAGTTAGTAAACAGGAGTATGGAGAGGCAAAATACAACTTCTTCTCTCAAGGACACGC 383

Qy 101 SerAlaGlyGluSerAspMetLysIleIleArqValLeuTrpTrpTyrTyrPheSerLys 120

Db 384 ACCGCGAGGAGATACAGATATGAAGATTATCCGTCCTCTCTCTCTCTCTCTCTCTCT 443

